

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120
 AACTTCGAA GGTATTAACA GCGAAGTATT AGAATATGCC GAnATTCAAG AATTTGATCA 180
 5 AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAAC TCATT AAATGTATnA CTACATGCAC 240
 GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300
 GGA 303

10 (2) INFORMATION FOR SEQ ID NO: 3090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60
 GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTTACA AATACTGAAC CAGCGTTCAT 120
 25 GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180
 TAATTCCTAA TKTATGTGGG ATTAACTTG GAAATTCAT TtAATGTAAC TTCATCAAAC 240
 CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300
 30 ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGGACGT ACTGAATGGA CCCTTTCTCG 360
 GnGTGTATCT GCAAGGTCAA TTTTCATTnT CAGGCATGGT 400

35 (2) INFORMATION FOR SEQ ID NO: 3091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

45 TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60
 TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120
 GATAGTCACG TAATGGATTT TGTGTGTCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180
 50 GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAAATCATA 240
 CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

(2) INFORMATION FOR SEQ ID NO: 3092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

CGACACCTCA ATAATCATAT CGTAATGTTT AACTTTTCCT GATTTAAATG TAATTTTCATT 60
 TCCATTGATA GCATTAAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC 120
 ATCAAGTATA GGTTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA 180
 TAAAGTAGGG TGTAACCAC GTTCCATAAA GATTTC AAGG AACTCCAATG GAACATAACC 240
 TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA 300
 TCCAGGGCCT CCAAATTC nAGGGGAAAn GGTAATATCC ACCTTCCAAG GCCAAGGGCC 360
 AATTGGCACC TGGCCACCCA GGGnCTTAAA AAGGGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 3093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

TTATACCCGn CAAATTCATA AATATAGTnC CTTTTCAATA GATTGATATG TATGTCTAAA 60
 TGTATCGATT AACTTTGCTA ATGCTGCTTC ATCTAATGGT CGGTCTGCTA ATTTTAAAAA 120
 TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTC TTTAGATGAT GGTTCGGTTA 180
 AGCCACATGC TTAAATGCA CTTTGTGTTG CTACTTCACC ACATTTTTTC GTGTCTGCCA 240
 ACGTACCATC AA 252

(2) INFORMATION FOR SEQ ID NO: 3094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60
 AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120
 5 TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180
 AGGTCAATAA TAAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240
 GGCCGAGGTA CAAAAAATGT TGAGCATTTT AAAGTATAAA CTTATCGACA CGnTTGTGTG 300
 10 CAGTTTTTCAT GTTT 314

(2) INFORMATION FOR SEQ ID NO: 3095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60
 25 ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAG CGTATTTAGA AAATGCCACG 120
 CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180
 ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAAnAAGTT GGACCCTTTG 240
 30 AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300
 GCTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

(2) INFORMATION FOR SEQ ID NO: 3096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60
 ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120
 TACATACTTT TGAAGTAGCT GTCTCATTTG TTGATTCATG TAAATGACAT CATGCTCCAT 180
 50 TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240
 ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTTC GTCCATATCC ACGGATGGCG 300

ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 3097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC | 60 |
| | CAATAATCCC nCACGATATA CGTGGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG | 120 |
| | ATGCACTTAC AATTTTAAAT AGATTTTAA GACCTTGTTG GTTTTGTACA ATTAATGTGA | 180 |
| 20 | CATGACTAGG TCTTGCACGT TTATATGCAT CTTCACTACT GAGTTTTTTG GTTGATTnC | 240 |
| | GTTATGATTT AATACGGCTA ATTCT | 265 |

(2) INFORMATION FOR SEQ ID NO: 3098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | CTAATGTATC AGTTTGGCAT GAATTCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT | 60 |
| | TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG | 120 |
| | ACCATTCTTT TTCCTTTTTC TCTTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT | 180 |
| 40 | CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGA | 240 |
| | TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTC TGACCTTTTA | 300 |
| | AAATCATTTnA CTGTCAnCAG A | 321 |

(2) INFORMATION FOR SEQ ID NO: 3099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60
 AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATTT TGTATTACCT GAAGTTTAA 120
 5 TTTCAACTGA TAATAATGGG ACATTTTAA CTTATACAGT TAAAAGGGAA AGTTTACTG 180
 TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240
 CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276

(2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAAACGTT 60
 GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120
 25 GCAAnGTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180
 AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

(2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

nCGATATAAC AAGGTTGTTA GACTTAAAGG TGGCGATCCA GCGATATTTG GTCGTGTGCA 60
 AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120
 ATCAGCGAGC GChAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180
 45 AAGTGTGGAC ATTTTCTACA GGTCACTTT AAAGATTCAG AAGAAAATGA AGTGGGATGG 240
 TCCATTCCTT AAGT 254

(2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

| | | |
|----|-------------------------------------------------------------------|-----|
| 5 | CAATCACTCA TGTAGTAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA | 60 |
| | ATGGCATAAT CTTCATnTGT AATGTTTAAT TTACCGCCAn TAACAGATAA GATATGTTGC | 120 |
| | ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCATCTA AGATGAATTT | 180 |
| 10 | ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT | 240 |

(2) INFORMATION FOR SEQ ID NO: 3103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

| | | |
|----|-------------------------------------------------------------------|-----|
| 20 | GTTGTAAACT TCAATTGTTC AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC | 60 |
| | AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG | 120 |
| 25 | AATTTTACTT GAATCAGGTG CTGAnACATA TCGAGTTGAA GATACAATGA ACCGTATCGC | 180 |
| | ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCAGT TCAACTGCAA TTATTTTTTC | 240 |
| 30 | ATTAAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG | 300 |
| | AAnGTGCGAA TAAGCGGGGn AATTCTTC | 328 |

(2) INFORMATION FOR SEQ ID NO: 3104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

| | | |
|----|-------------------------------------------------------------------|-----|
| 40 | TTTTGCTTTG TCGCTAATA ATCTAATGTT CGTGGAACCG nAACCAGAGA TATTACAAAT | 60 |
| 45 | ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG | 120 |
| | CTGATTTAAG GCGGCATTGC AAAACTATTC GCCACGAATC CTGAACGTCC TTTGCCAGCT | 180 |
| 50 | ACAAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACTCA TCCGCTTCAA | 240 |
| | CATGTGACAA AGTCACTTTA ATCnA | 265 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60
 ACTGGAACTA CTAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120
 nGTATTGGAC GTGGATCAGT TGTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180
 AAGGTAAAGA TTTATCTGAC AAATTGATCG TTACTAACTC AATCGATGAA ACGTTTGTGA 240
 CCT 243

(2) INFORMATION FOR SEQ ID NO: 3106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60
 AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGnG CCCAAACACA TCTAGATGCT 120
 TTACTAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180
 CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

(2) INFORMATION FOR SEQ ID NO: 3107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60
 CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTGAACGT GTCCAAAATA 120
 GCGGnTAGAn ATTCTTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

(2) INFORMATION FOR SEQ ID NO: 3108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60
 TCTAATTGGA TACAATGTAA ACAAATGGT GnATTTGTAT TATAGATAAT AAACATTcGn 120
 TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180
 CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240
 AGTATTATGC AAGTACT 257

(2) INFORMATION FOR SEQ ID NO: 3109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCCT GAATCTTGCA ATGCCTTTTG 60
 TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120
 ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180
 TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

(2) INFORMATION FOR SEQ ID NO: 3110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTTAATTGGG AAAnCAGGTA AAAAGGATGG 60
 AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCCnCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240
 CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300
 5 CnAAGCGCGT ATTAGCACTA GCCGAA 326

(2) INFORMATION FOR SEQ ID NO: 3111:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTTATCA 60
 20 ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120
 ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180
 ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT nAATTTTTTA 240
 25 TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

(2) INFORMATION FOR SEQ ID NO: 3112:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTTAA CACAAGGnTT CGAACAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60
 40 AGCATTTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120
 TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180
 GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTA 240
 45 TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300
 CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

(2) INFORMATION FOR SEQ ID NO: 3113:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTCGAATC CCTCTTCCTC 60
 5 CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT 120
 ATTTACCTTT TTTATTTGTC TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG 180
 CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAAATACAT AGCAAAATGT CGTTGTTGTT 240
 10 TTGTGATAGA T 251

(2) INFORMATION FOR SEQ ID NO: 3114:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 6591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

TTTAAGTGAA TTnCTTTGGG TTACAGAAWT TTCAACAACT TTAAAGCAGC TATAATGATG 60
 25 ATTTTCAGCT TGTACAAAGG AGAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC 120
 GCCTAATAAT AAAAActCTA AAAGTTGTAT TTTAAAAATA GTTCTTTAAA TTATATACCC 180
 ACCACATTTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAActTCCA ATATTGAACT 240
 30 CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTTGAGTC CACTTTTATT 300
 TGTATTGTAT AGAGAGAAAT AAAAAGAAAC CTTGTTTTAC AAGGTTTCTA ATACGTTATG 360
 TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACACT CCACAAGTGG 420
 35 AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCCGCCAC ACCGGCTTAA TGGTAAACAA 480
 AAAActTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT 540
 CCGGAAGGA ACGTGtTCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG 600
 40 AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA 660
 CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC 720
 GGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG 780
 45 ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA 840
 TAACTGGGCT AGCTGGATTC GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG 900
 50 CTTGGCTATA GCCCATTAAT AATAAGGGCG GCTGAAGGGG ATCGAACCTT CGAATGTCGG 960

55

| | | |
|----|-------------------------------------------------------------------|------|
| | CGAACCCACA CCAAAGGTTT TGGAGACCTC TATTCTACCG TTGAACTATG CCCCTATTAA | 1080 |
| | AAATAATAAA TGGAGGGGGG CAGATTCGAA CTGCCGAACC CGAAGGAGCG GATTTACAGT | 1140 |
| 5 | CCGCCGCGTT TAGCCACTTC GCTACCCCTC CATAAATGGT GCCGGCCAGA GGACTTGAAC | 1200 |
| | CCCCAACCTA CTGATTACAA GTCAGTTGCT CTACCAATTG AGCTAGGCCG GCTAAGAAAT | 1260 |
| | GGTTCAGGAC AGAGTCGAAC TGCCGACACA TGGAGCTTCA ATCCATTGCT CTACCAACTG | 1320 |
| 10 | AGCTACTGAA CCATAATAAA AATGTAATGA TGGCGGTCTC GACGGGAATC GAACCCGCGA | 1380 |
| | TCTCCTGCGT GACAGGCAGG CGTGTTAACC GCTACACTAC GAGACCTATA AAATATTGCG | 1440 |
| | GGAGGCGGAT TTGAACCACC GACCTTCGGG TTATGAGCCC GACGAGCTAC CGAACTGCTC | 1500 |
| 15 | CATCCCGCGA TAATAAAAAA TAATGGCGGA GGAAGAGGGA TTCGAACCCC CGCGGCCCGT | 1560 |
| | TAAGGCCCTG TCGGTTTTCA AGACCGATCC CTTAGCCGG ACTTGGGTAT TCCTCCATTA | 1620 |
| 20 | TTATAGGTAA ATCGCTATTA ATTATAAAAT TAAATGGCGG TCTCGACGGG AATCGAACCC | 1680 |
| | GCGATCTCCT GCGTGACAGG CAGGCGTGTT AACCCTACA CTACGAGACC ATTAGTAAAA | 1740 |
| | CGGAGGAAGA GGGATTCGAA CCCCCGCGAG CCGTTAAGCC CCTGTCGGTT TTCAAGACCG | 1800 |
| 25 | ATCCCTTCAG CCGGACTTGG GTATTCCTCC AAAATTATAT GGaCtTGCAG GACTCGAACC | 1860 |
| | TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA | 1920 |
| | ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG | 1980 |
| 30 | AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAA TAATATGGTG | 2040 |
| | GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAA GCAGGCGCTC TCCCAGCTGA | 2100 |
| 35 | GCTAAGCCCC CATAATAATT ACAGTATATC GGAAGACAG GATTCGAACC TGCGACCCCT | 2160 |
| | TGGTCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA | 2220 |
| | TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG | 2280 |
| 40 | GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAcGgTGATC | 2340 |
| | ACTCACCGCA GGATTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA | 2400 |
| | AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TGTATTCTAC | 2460 |
| 45 | CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACgCC GTAAGGCGCT | 2520 |
| | aGATCCTAAG TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG | 2580 |
| 50 | GATTCGAACC TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGA GCTAATGGCT | 2640 |
| | CTTCCATGGT GCCGGCCAGA GGACTTGAAC CCCCACCTA CTGATTACAA GTCAGTTGCT | 2700 |
| 55 | CTACCAATTG AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA | 2760 |

| | | |
|----|--------------------------------------------------------------------|------|
| | AAACTGCCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG | 2880 |
| | GAGCTTAACT TCTGTGTTCC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA | 2940 |
| 5 | CATATGAATG TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGtGnA TTTTgctCGC | 3000 |
| | AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC aCATGTCACC | 3060 |
| | ATGCTTCCAC CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTATA ACCGAAGTTG | 3120 |
| 10 | GGAAATCTCA TCTTGAGGGG GGCTTCATGC TtnAgGATtT TCAGCACTTA TCCCGTCCAC | 3180 |
| | ACATAGCTAC CCAGCTTATG CnTTGGCACG ACAAcTGGTA CACCAGAGGT ATGTCCATCC | 3240 |
| | CGGTCCTCTC GTACTAAGGA CAGCTCCTCT CAAATTTCTT ACGCCACGA CGGATAGGGA | 3300 |
| 15 | cCGAACTTcT aCGACGTTCT GAACCCAGnC sTGTACCGCT TTaATGGGCG AACAGCCCAA | 3360 |
| | CCCTTGGGAC CGACTACAGC CCCAGGATGC GATGAGCCGA CATCGAGGTG CCAAACCTCC | 3420 |
| 20 | CCGTCGATGT GAACTCTTGG GGGAGATAAG CCTGTTATCC CCGGGGTAGC TTTTATCCGT | 3480 |
| | TGAGCGATGG CCCTTCCATG CGGAACCACC GGATCACTAA GTCCGTCTTT CGACCCTGCT | 3540 |
| | CGACTTGTAG GTCTCGCAGT CAAGCTCCCT TATGCCTTTA CACTCTATGA ATGATTTCCA | 3600 |
| 25 | ACCATTCTGA GGGAACCTTT GAGCGCCTCC GTTACCTTTT AGGAGGCGAC CGCCCCAGTC | 3660 |
| | AAACTGCCCCG CCTGACACTG TCTCCCacca CGATAAGTGG TCGGGGTTAG AAAGCCAACA | 3720 |
| | CAGCTAGGGT AGTATCCCAC CAGCGCCTCC ACGTAAGcTA GCGCTCACGT TTCAAAGGCT | 3780 |
| 30 | CCTACCTATC CTGTACAAGC TGTGCCGAAT TTCAATATCA GGCTACAGTA AAGCTCCACG | 3840 |
| | GGGTCTTTCC GTCTGTGCG GGGTAACCTG CATCTTCACA GGTACTATGA TTTCACCGAG | 3900 |
| 35 | TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTTCGT GCGGGTCGGA ACTTACCCGA | 3960 |
| | CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCGA | 4020 |
| | TTCTAGCTT CGCAGAAncT ArCcACTCCT CTTAACCTTC CAGCACC GGG CAGGCGTCag | 4080 |
| 40 | cCctATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA GTCGCTTGGG | 4140 |
| | CCTATTCAC T GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG CACCCCTTCT CCCGAAGTTA | 4200 |
| | CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG CTCACCTTAG AATTCTCATC | 4260 |
| 45 | TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT CTATCTAGAG GCTTTTCTCG | 4320 |
| | GCAGTGTGAA ATCAACGACT CGAAGACACA ATGTCTTCTC CCCATCACAG CTCAGCCTTA | 4380 |
| | ACGAGTACCG GATTTGCCTA ATACTCAGCC TTAGTGCTTA GACGTGCAAT CCAATCGCAC | 4440 |
| 50 | GCTTCGCCTA TCCTACTGCG TCCCCCATC GATTAAAACG ATTATAGGTG GTACAGGAAT | 4500 |
| | ATCAACCTGT TATCCATCGC CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCAG | 4560 |

55

| | | | | | | | |
|----|------------|------------|-------------|------------|------------|-------------|------|
| | TTCGCTACTC | ACACCGGCAT | TCTCACTTCT | AAGCGCTCCA | CATGTCCTTA | CGATCATGCT | 4680 |
| | TCAACGCCCT | TAGAACGCTC | TCCTACCATT | GTCCAAAGGA | CAATcCACAG | CTTCGGTAAT | 4740 |
| 5 | ATGTTTAGCC | CCGGTACATT | TTCGGCGCag | TGTCACTCGA | CTAGTGAGCT | ATTACGCACT | 4800 |
| | CTTTAAATGA | TGGCTGCTTC | TAAGCCAACA | TCCTAGTTGT | CTGGGCAACG | CCACATCCTT | 4860 |
| | TTCCACTTAA | CATATATTTT | GGGACCTTAG | CTGGTGGTCT | GGGCTGTTTC | CCTTTCGAAC | 4920 |
| 10 | ACGGACCTTA | TCACCCATGT | TCTGACTCCC | AAGTTAAATT | AATTGGCATT | CGGAGTTTGT | 4980 |
| | CTGAATTCCG | TAACCCGAGA | GGGGCCCCCTC | GTCCAAACAG | TGCTCTACCT | CCAATAATCA | 5040 |
| 15 | TCACTTGAGG | CTAGCCCTAA | AGCTATTTTCG | GAGAGAACCA | GCTATyTCCA | GGTTCGATTG | 5100 |
| | GAATTTCTCC | GCTACCCTCA | GTTTCATCCGC | TCACTTTTCA | ACGTAAGTCG | GTTTCGGTCCT | 5160 |
| | CCATTCAGTG | TTACCTGAAC | TTCAACCTGA | CCAAGGGTAG | ATCACCTGGT | TTCGGGTCTA | 5220 |
| 20 | CGACCAAATA | CTAAACGCCC | TATTCAGACT | CGCTTTCGCT | ACGGCTCCAC | ATTTACTGCT | 5280 |
| | TAACCTTGCA | TCAAATCGTA | ACTCGCCGGT | TCATTCTACA | AAAGGCACGC | CATCACCCAT | 5340 |
| | TAACGGGCTC | TGACTACTTG | TAAGCACACG | GTTTCAGGTT | CTATTTCACT | CCCCTTCCGG | 5400 |
| 25 | GGTGCTTTTC | ACCTTTCCCT | CACGGTACTG | GTTCACTATC | GGTCACTAGA | GAGTATTTAG | 5460 |
| | CCTTAGGAGA | TGGTCCTCCC | AGATTCCGAC | GGAATTTTAC | GTGCTCCGTC | GTACTCAGGA | 5520 |
| | TCCACTCAAG | AGAGACAACA | TTTTCGACTA | CAGGATTATT | ACCTTCTTTG | ATTCATCTTT | 5580 |
| 30 | CCAGATGATT | CGTCTAATGT | CGTCCTTTGT | AACTCCGTAT | AGAGTGTCTT | ACAACCCCAA | 5640 |
| | CAAGCAAGCT | TGTTGGTTTG | GGCTCTTCCC | GTTTCGCTCG | CCGCTACTAA | GGGAATCGAA | 5700 |
| 35 | TTTTCTTTCT | CTTCCTCCGG | GTACTAAGAT | GTTTCAGTTC | TCCGGGTGTG | CCTTCTGATA | 5760 |
| | TGCTATGTAT | TCACATATCG | ATAACATGAC | ATAACTCATG | CTGGGTTTCC | CCATTCGGAA | 5820 |
| | ATCTCTGGAT | CAAAGCTTAC | TTACAGCTCC | CCAAAGCATA | TCGTCGTTAG | TAACGTCCTT | 5880 |
| 40 | CATCGGCTTC | TAGTGCCAAG | GCATCCACCG | TGCGCCCTTA | ATAACTTAAT | CTATGTTTCC | 5940 |
| | ATCCTACAGG | AAACGCGTTA | TTAATCTTGT | gaGTGTTCTT | TCGAACACTA | GCGATTATTT | 6000 |
| | CTTATGAATT | CAAGCTTATT | TAAAACTCTT | TATTCACTCG | GTTTTGCTTG | GTAAAATCTA | 6060 |
| 45 | TATTTTACTT | ACTTATCTAG | TTTTCAATGT | ACAATTTCTT | TTTAGTCAAG | CGCTCGCATA | 6120 |
| | AGCAATATCA | CTTTAACCBA | AAAATATTTG | AATGTTAAAT | AAACATTCAA | AACTGAATAC | 6180 |
| 50 | AATATGTCAC | ATTATTCCGC | ATCTTCTGAA | GAAGATGTTT | CGAATATATC | CTTAGAAAGG | 6240 |
| | AGGTGATCCA | GCCGCACCTT | CCGATACGGC | TACCTTGTTA | CGACTTCACC | CCAATCATTT | 6300 |
| | GTCCACCTT | CGACGGCTAG | CTCCTAAAAG | GTTACTCCAC | CGGCTTCGGG | TGTTACAAAC | 6360 |
| 55 | | | | | | | |

ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480
 GAGAACAACCT TTATGGGaTT TGCTTGaCCT CGCgGGTTTCG cTkGCCTTTG TAATGTCCAA 6540
 5 TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

(2) INFORMATION FOR SEQ ID NO: 3115:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60
 20 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120
 TGTAAATTGTT TGTGTTTACG TATTTCTGGT GTAAGTTCCG TGAAACCAAT GTCTATATTC 180
 CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240
 25 TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCAa TCCCCnCCAA 300
 GCCCATnGAG GTACCTTTAA TTTTA 325

(2) INFORMATION FOR SEQ ID NO: 3116:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

40 CCGnTTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60
 GnTTTACCTA CTAAATTTGA GGCGGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTCA 120
 GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180
 45 TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

(2) INFORMATION FOR SEQ ID NO: 3117:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGTnTTTT GAAATGATTG CGGCGATGTT GGCGACAGTT AAAGTAGGTG GCATCTTATA 60
 5 TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120
 TAACTGCAGT CATGTCTTAC GGCGTTGnAA TTGAAACGAC ATTACCAGTC ATTCAATTGG 180
 AAAATGCTAA AGGCTTTGTT GAATCAAAGG 210

(2) INFORMATION FOR SEQ ID NO: 3118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60
 GTTGCCATT C AACACTTGAT TAATTTTCAGT TAACTTTTGA CGCGCTGCTT GTAATTTTGT 120
 25 GGTGTACGCA TTTAACGAAC GGnCGTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180
 GTTCTAAATT GCGTTTCCAA GTTnAAGCG GCGCTTATCT GGTGT 225

(2) INFORMATION FOR SEQ ID NO: 3119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTAG 60
 CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120
 GAGTGCGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180
 45 GTGTGTTGAT GnCGAnCACA ACCCCTCCGA ACACGCTTAA TG 222

(2) INFORMATION FOR SEQ ID NO: 3120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

5 CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60
 GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120
 TACGATTCCT GTTTATATGC CATATATCAC ATCTTATTTT ATGGACGCGT GCTATCGGCG 180
 nACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240
 10 ACTTTG 246

(2) INFORMATION FOR SEQ ID NO: 3121:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

25 CAAATACCTT CTCAACnTTG TACTTTTTTGC CTAATTGAGC TGCACGAATT GCTGCAACGT 60
 ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACCTAC 120
 CATGTTTTAC CCCTCCATTA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180
 CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGAkrtGct 240
 30 AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTTGAGC AATACGGCCA 300
 ATTCCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360
 35 TGAACCGATA TTACTGATTG TGCATnnGCA CCTTnCATT 399

(2) INFORMATION FOR SEQ ID NO: 3122:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

45 CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60
 TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120
 50 ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180
 AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

55

G

301

(2) INFORMATION FOR SEQ ID NO: 3123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT | 60 |
| | AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAATCGGC GAATATCTGA ATTCAAAACC | 120 |
| | AGCGATTATC ACAGCAATTA TTTAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG | 180 |
| 20 | TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCACT AGCTTGCTTA ATGATGCACT | 240 |
| | TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA | 300 |
| | TCGTnGGCCn ACGTTAACTA ATTCnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA | 360 |
| 25 | GTACGCCAAC TGCCACGA | 378 |

(2) INFORMATION FOR SEQ ID NO: 3124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TATTGCAAGA AATGAACTGC TGATTTTTAT AGTTTTAGTG GTCATAAAAT GCTTGGACCA | 60 |
| 40 | ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG | 120 |
| | TTCGGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC | 180 |
| | TACTAAATTT GCAGGTCGGG TTACTCCCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG | 240 |
| 45 | CnAGGAAGCC T | 251 |

(2) INFORMATION FOR SEQ ID NO: 3125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA 60
 5 TCCATACGTT CGATTTTACT CTTCGCATTT TTAATGTTAG TTGCAATTTC ACGTTGAACT 120
 AATTCTTTCA TTACGAATGG TTTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT 180
 TGGTACCATT TCCAnGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA 233

10 (2) INFORMATION FOR SEQ ID NO: 3126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGTACCTT GTTGTnCTCC ATTGGCAATG 60
 TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTTG ACGTGCTTTA TTTTACAGCA 120
 25 TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC 180
 AATCACATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCTTGAT AACTTTGCAC 240
 TGTCGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA 300
 30 TGTCTTAACA TTATCGACAA CGGTGCCTTG TAACCCTTCT GTCAATGTCA GTTGTTCAAC 360
 TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA 413

35 (2) INFORMATION FOR SEQ ID NO: 3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

GTCGTAAATA CTGAACAAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA 60
 CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG 120
 50 TAnATCATCT TCTACATACA TAGGTAATTT TATGGCGATT CCTCATGGAG CATCCTGTAA 180
 AAAGTTTAC AATCACATGT GCTTATTTT 209

(2) INFORMATION FOR SEQ ID NO: 3128:

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

10 TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC 60
 TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTTGGTAT 120
 ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG 180
 15 CCTTCnAAAA ATATGCTGAA AGnC 204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA 60
 30 AATCTTAACT TATCGAAGTA TCCTGTTTTT TCTGCAACAC CAATACCAAT CATCACTGCT 120
 AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTTTAAT CGTATTCTTC TTATCATCGT 180
 AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC 239

35

(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT 60
 AATATATTCT CTnGTCTCAA CCTTAATCGT AACTTCAGA CGTCTGTTTG TAGACAATAA 120
 50 AGTCATTCAC GTCTTCATAT GTCATCAnAT GTTTATCATG ATATGATGAT ATATAATCGG 180
 TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG 240
 CTGAGAGCTG TGTATCAGT 259

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60
 TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120
 CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180
 CTTGTnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

(2) INFORMATION FOR SEQ ID NO: 3132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGTnATCATC TGCTGCTGTA GChTAGCAGG TTCAATTTCA TTTATCGGAT 60
 TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAGTTG TATTAACCAA 120
 TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180
 TTACAACCAG GTGGGGTTCC AGC 203

(2) INFORMATION FOR SEQ ID NO: 3133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGGTA GCTGGCACAG ATATTACGAA 60
 TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120
 AGGTTATGTC AAACTGAATT ATGGTTTTCh AGTGCTAATT CTGCTGTAA GGTGACACAT 180
 TCAAAATACT GTACCTAAGG A 201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60
 CGAAAGAGGT ACCGnCGAAT ATTCACAAG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120
 AATCATCATT CTTTATGCAT TAGGATTTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180
 AGCGGAGGTA TTTTAAAATT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60
 GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTTCGG TGTTAGCGGT GGAGTGCAAn 120
 TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180
 CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCAnTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60
 AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTTGA 120
 ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180
 TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

ATTGGGAAAT GTTCCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG 60
 GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAGTTGnA 120
 AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT 180
 TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA 240
 AGAATCCTGC CTTACCTAAG 260

(2) INFORMATION FOR SEQ ID NO: 3138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTGTGATTA TCATTGCTT 60
 TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCATT ACTTTCACCTA TTATCTTCAA 120
 GCGATAATTT CTTAACTGCA CTTACCACTT GCTCAATTGC TTCTGCTAT TGTCATTCTGA 180
 TATCGGAGTA GTAGGAAGTG CnGAATTCGG CA 212

(2) INFORMATION FOR SEQ ID NO: 3139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT 60
 TGAATATGTTG CGACGCTTAG ATCACAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA 120
 TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA 180

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300
 GAATATGGTA CAAATGTTTT AACAAATGGCA CAAAGATGCA ATTGAAACCA GGTnCAACGT 360
 5 GTGTTAnTAC AGG 373

(2) INFORMATION FOR SEQ ID NO: 3140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60
 20 TCGTTTTGTA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120
 CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180
 ACCnTGCCCC AACTAAAATG GCATTGGGTA AAACCACnTG 220

(2) INFORMATION FOR SEQ ID NO: 3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60
 ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120
 40 TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

(2) INFORMATION FOR SEQ ID NO: 3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTTAGC ATTTGGTTTA ACAACnGGT GTTGCAAGTAT CCCCACnTAA GGTCTGTATA 60

ATTTCAATTTT TATGTTTCCTC GATAACTTGT ATTGCTGCTT GTTTTCCTCC ATCTGTCAAT 180
 CCATCATTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60
 ACTGACTGAG CCATAAAATG CGAAAGTTAC TGCGCCATAT AGACTGATTA ATCATATGTC 120
 ACCATTGGAT TTGGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180
 AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGTT TTTGAAATGG GCCCACGGGC 240
 TTGTTTAAAT CAAAATTAAA AAATTGTGGT nCTTGGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60
 CAGTAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120
 GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCtATAGT ATTTGTAACC ATCTTTTAGT 180
 TGATaAATGC CACGCGCATC TGTTATTGCG TCATTTTtag GTAcAAATTG AATTTkGAGA 240
 TTTCTCaCaT TATCAGGTAC TTAAATAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300
 TCAGCAATCG TATCATTAGT ATCAGCATTT TTGATAATAA CATTTGTTGC GCCTTGACCG 360
 TTTTtagTAG TCATTGTATT AAATCAAGGT TAATTCAGAA TTCGGATTTA CTGTAAATGC 420
 TTTCTCGATA CCATTAAAAT CGCCATGGTC ATTCGTATCA GTTCCAGTAT ACGGCCTAAT 480
 GCAATACATT TGCCTGTGCh TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

(A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

10 ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTC 60
 ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120
 TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180
 15 TAACCATAGT TTGGTTGGAT CAAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240
 TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCCTGGTA ACCATGGTGG TGGTAATAAC 300
 CC 302

20

(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

30 CAGGAATAGG ATCATTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60
 CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCCT 120
 35 CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180
 AACCAATCCA CTTTCTACCT GGTTTCCGGT AAATTTTAC CTCCATACCA GGGnCCCTCCC 240
 CCTTTTTTGG GCCAAAATAG GAAAAAnGAG GCGGGGGAAA TCCTCCCCC AATTCCnTTC 300
 40 CTGGCCCTGG AGGTTTCCAC CTAAATTTTT TT 332

40

(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

GAGAGTGGTT AACAAGCAAA TAGAAATAAT TAAAATGCA GATGCAGATG CATCGGCGAA 60

55

CnCCAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180
 TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTGGCC TTTGGATTTT AAGATATTGG 60
 TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120
 CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180
 TTTTGTTCa GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60
 TTATGGCTAT CATTTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120
 TTGTTCCAT GATAGGTCAC GATTATTAAa AGTGCATTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60
 TCTGGCGGTA CCATTACAG GTACCGCAGC TTATTAAAGC AACATCACGG GCAATGTTAT 120

A

181

(2) INFORMATION FOR SEQ ID NO: 3151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTAAATTG AGCGACATAC TCTTCTGTTA GCTCTGCTAC TTTTAAAT AGAGCGATTG 60
 ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120
 CTAATAAAT AATTTCGAAT GCTATCATTG GTTGTTTCAA CAGCTTGATG CT 172

(2) INFORMATION FOR SEQ ID NO: 3152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTTAT AAGCGATATA GATTTCGCAT GTTGCATTTA TTAAACCTAA 60
 TAATGGTAAA CGACAAGTGT GACTGTTACT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120
 AAATCAACCA AAAGTAGGTA TTTGAATTTT GGAATAATG AGACATAGCG AGAGTGTATA 180
 TGCAATACGA CAGTACTTTA AATTAAGAG 209

(2) INFORMATION FOR SEQ ID NO: 3153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60
 TTGCCTAAAG GTTCAATCGT TAAACCTTCC AATAAATTTG CTGTTGCTGG ATAAGGAGAA 120
 ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

| | |
|-------------------------------------------------------------------|-----|
| GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG | 60 |
| GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA | 120 |
| ACTTAAGAGC AATGTTTGCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTGCGA | 180 |
| AACTTTACAA TATTTGTTGC GGATGATTAT TTAACTTTGT GAGAATGTTG ATGGCACAGT | 240 |
| CCACTATAnC AATCAGTATC GCAATGG | 267 |

(2) INFORMATION FOR SEQ ID NO: 3155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

| | |
|--------------------------------------------------------------------|-----|
| AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCTCTC AAGAAGCAAA | 60 |
| TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT | 120 |
| TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA | 180 |
| AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG | 240 |
| GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT | 300 |
| TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA | 360 |
| AATTTTACAG TGACAGATAA gTGAAAyCAG GGgATTATTT TmCacGAgTT ACCAGATatT | 420 |
| TAcTGGTAAT GGAGACGTGG GATTATTCTA ATTCAnATAA TACGATGCCA ATTGCAGACA | 480 |
| TTAAAAGTAC | 490 |

(2) INFORMATION FOR SEQ ID NO: 3156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CCTTCAGTAC CTTGTAATAG TTAnTTAAAT GTTCCGATCA TCGTGTAGTG TGATTCATCA | 60 |
| 5 | TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT | 120 |
| | TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTTTTTC AGATAGCATC ATTGGTGGAT | 180 |
| | TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT | 240 |
| 10 | TGGCGCACAA TCCnTGCACC GT | 262 |

(2) INFORMATION FOR SEQ ID NO: 3157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT | 60 |
| 25 | TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTTGAGCTT CTGCTGTCGT TTTAGCCATT | 120 |
| | GGGTTTTTCAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA | 170 |

(2) INFORMATION FOR SEQ ID NO: 3158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

| | | |
|----|-------------------------------------------------------------------|-----|
| 40 | CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA | 60 |
| | ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT | 120 |
| | ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG | 180 |
| 45 | CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG | 240 |
| | GCAGTTTATA GACATACATT GTGnCCTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG | 300 |
| | TACAGTAAGT An | 312 |

(2) INFORMATION FOR SEQ ID NO: 3159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60
AATATCTAAT GTTTAAAATC TATCGTCGCA AGATGCTTCC TGnTAATTAT CAGTGCCATT 120
TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

CTTGTTTCATT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60
CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATTT 120
CACTGGTAAT ATTTCTGTTCA TTAATCnTGA TTGAGGGAAT TCCGCCCATC CAGAnGTCCC 180
CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

30

(2) INFORMATION FOR SEQ ID NO: 3161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

GCACAGGTAG CGGTAGTGGC GGTCGTATGA TGACTTTGGT AATCTAAAGC AAAATGTACG 60
ATAATAATAA ACGTCGTTTC GTTTCTCTGA TGTAGCAGGG GCAGTGAAGA AACAAGATTA 120
TTGAATTGTT GATTTCTTGA AGATATAAAA ATTCAAGAAT GGGTCTAGGA TTCCTAAGGT 180
GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240
CTCTTTTGGG TCAGnTTTGG AGTTTTGTTT GTCGGCTGTC GGATThTCGT ATGTAGGAAC 300
GGCTGTTTAC TTnCGTGGAT G 321

50

(2) INFORMATION FOR SEQ ID NO: 3162:

55

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

10 AACATTGAG CAATATCAAG AACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60
 TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGTT TATTGCGGCG 120
 ACACTTTAC GAGGCGTGCA CTTTATACAA GTGCCAnCG 159

15 (2) INFORMATION FOR SEQ ID NO: 3163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

25 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60
 TTTTAAAGCT TGAAATTTAA CAAATCATAA GCCGTATGAA TATTAAATA TGCCACCATG 120
 ATTGAATGGC CCCTTTCTAT TAGTTAnGTT TTGTGCG 157

30

(2) INFORMATION FOR SEQ ID NO: 3164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

40 TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60
 ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCAT AGGTATTTCA TCAGCAGGnG 120
 45 TTGTTGATGA ACAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180
 ATTTTAAGGA TTATTAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

5 AGAAACACTT CTATTGAATC GTCTTACTGC TGTCTCTAT TTATAACACT TCGTATTGAA 60
TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTC CTAATGCCTG GATCCTTTAT 120
ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

10 (2) INFORMATION FOR SEQ ID NO: 3166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60
CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120
25 AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

(2) INFORMATION FOR SEQ ID NO: 3167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

TGTGGGGGAA ACCTGCACAG CAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60
40 TAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120
ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

(2) INFORMATION FOR SEQ ID NO: 3168:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

55

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120
 GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

(2) INFORMATION FOR SEQ ID NO: 3169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGAAAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60
 ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAAA CTGCATGCTT GCTCGATTGG 120
 CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAATT TAGTATGTCA AATGTCCCAA 180
 TCAnTAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60
 TCTAATTCTT GATGGAGGTG AAAACTGTTA ATTTTCATGTC CAGTAATGAT GATAGGCTGC 120
 TTCGCTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180
 GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTTTCAG AGATTGCGAC ATCGATTGGT 240
 AAATGTAAAt GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTTCG 300
 GTTGTTGCAT TTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTCG 360
 ATAGTCGTCA AATGTACCnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

5 TAGAAGGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TGCGCCAATT GCAGTGTGTA 60
 ACGAGCGACC AGAATCACTA TTTAATTACT TTAAACAGCT GTTTGCACAA GTTACGAATC 120
 CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180
 10 AAGGTAACCTT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCGG 240
 TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTAAATT AACTTATTTA 300
 TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360
 15 TGAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

(2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

25 ACATAATTTA AAATAATATT ACATTTGTAA TGGnCACCAA GTAACGTTTC GGTTGCTTGG 60
 30 TGTTTTTTGG TATGAATTAC TTTCTGTTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120
 ATTAAGATTT AATTACAAAC GGAAACTAAA TGTAATAGAA TAAACT 166

(2) INFORMATION FOR SEQ ID NO: 3173:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

45 ATAATGAGAn TGTTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60
 CGAAAGACCC AACTCCAGGG ACCGCCGGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120
 GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

(2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60
 AACGTTTGAA TTTAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120
 TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

(2) INFORMATION FOR SEQ ID NO: 3175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

TATTTGAAGA TGGCTGTGTA CAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60
 ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCnA GTATGTCGTC AGAGAAGATA 120
 CACCTAATCG CTAATTAATG AGGTTTGGAA ACAT 154

(2) INFORMATION FOR SEQ ID NO: 3176:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCCTTCAG CCCATACGnT 60
 GCGAAAGGTT TATTAATTTT TTCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120
 ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180
 GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CGGTGCAATG 240
 GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGGTTATTC TGTTGAAGTA 300
 ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360
 CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420
 CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

(2) INFORMATION FOR SEQ ID NO: 3177:

(A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

10 TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AnTTGTCATC TGTGCTGGTG 60
 CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTAGTAT CTAAAACTT GAAAATATTC 120
 AAATCAATTG TTGGTGAAGT AATGGCATCA 150

15 (2) INFORMATION FOR SEQ ID NO: 3178:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

25 TTACTCTATC TTGATTTGAC GAAATACTAT TAnGCTAATA TCGATATTTT AAAAACGAGA 60
 TGATGTTCCA AAGCAAGCCA TTTCGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120
 30 TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

40 CTTGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60
 ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120
 45 TTAAAGCAGA TTTACGTATG TCTACAAGTT TAnTTGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCCnTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60
 5 GGTGTATTTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCATTCA 120
 TGATTGGGGC GATTTCGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180
 GTATTTATTT GGGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240
 10 TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

(2) INFORMATION FOR SEQ ID NO: 3181:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60
 25 ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120
 CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180
 CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACCTA CCGGTTCAAC TTGGTCGATG 240
 30 TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTGT 300
 TTnCACCGnT TnCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

(2) INFORMATION FOR SEQ ID NO: 3182:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

45 TACCAACACG TACACCTTCT AAAATAACTG CATTTGCACC GTnTTAATAC ATCATCCTCG 60
 TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120
 ACATGTACAT TTTTACCAGT TGTAGCAGC 149

(2) INFORMATION FOR SEQ ID NO: 3183:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

GCGGTGCCGG TGTGCAATT GCGCAGTGG TGTGGTAGC ATGTGGTCTT TCAATCAATG 60
TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120
ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTTGTTTCATA ATTCTCTGTT AAAGAACGAC 60
TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAACAGT GACATTTTCT CAATCGGCGT 120
ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCCAC GCTAGTCGnC 180

(2) INFORMATION FOR SEQ ID NO: 3185:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60
CCGTGCTACA ATCGGGnCAA GTTGGAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120
CCGGCACGTT CAAGATGGGA AAGGTATCCG 150

45

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

GAATTTnAGG TGAATCAGAA GATTAACGCT GTTGCCTCCT AAGCTAACAG ATACTGGTTC 60
 GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTTAATAAA ACCGTAACTC GAGCATTATT 120
 5 AGAGGAAGCT AACCAAAGCA GGTTTA 146

(2) INFORMATION FOR SEQ ID NO: 3187:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60
 20 AAATGGTGTC ATGTATTCAA CAGTCTGTTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120
 AAGGTCGGAC CGTTTGCGCA ATTGAGACCA GCGCGCAAT TAGGG 165

(2) INFORMATION FOR SEQ ID NO: 3188:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60
 35 ACATTCTTTG GTGTAAACGn AACCAATTTT ATTTGGTGCC ACCACTAGTT ATTGGAATCC 120
 TGTGTTCTTT ATTCCATTTG TATTAGCACC AATTGTAAAC GTATGG 166

(2) INFORMATION FOR SEQ ID NO: 3189:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

50 AACCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60
 GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTTATCTA ATTGATCCTT ACCAGTTTGA 120

(2) INFORMATION FOR SEQ ID NO: 3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTTGGGAAA AATTTTTTAA CCCCCCTTAA 60
 AnTTCCCGGG AAAAAGGAAA CCCGGGTTTT TAAAAAAAC CCGGGGTTCC CAAAAATTTT 120
 TTGGGAAAGG GAAAGGAAAA AAGGGTTAAA AAATTTTGG GAAAAACCCG GGCCCAAAAA 180
 AAAGGGTTTT TTTCCCCTTA AAAAAAATTT AA 212

(2) INFORMATION FOR SEQ ID NO: 3191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TTGCCCTTAC AACGATAGCT AATGATTTAT 60
 ATTGTAACT CAATGACCT TGTGAATAC CTTCTGACAC AAGCGCGCGA CATGCTGCAA 120
 AGTTTTGCGC TAAACCAACG GCAGCAAC 148

(2) INFORMATION FOR SEQ ID NO: 3192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTAA TTAAACCAGC TGCTTCTAAT AGTTTAAGTG 60
 CACGTGCTTG GTTTGACACA TCATTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120
 TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCAGG GATGGCTCTT AAATATATGT 180
 TACGTGATAA TTTCTCGAnA AATGGCTTCC CT 212

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTTGGATACT GGTTATATTC AGCTGCACCG 60
 CAAGCAACTT CTATTGATGG CCAACTGCC TTTTACCTC AAGCAATGGG TATGGTAGTT 120
 GTTGCAGTCA TTTATGGCTT T 141

(2) INFORMATION FOR SEQ ID NO: 3194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACG TTC TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCTG TGGCGGAATG 60
 GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120
 GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAAA ACCTCAGCCT 180
 TCCAAGCTGA TGTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240
 ATTGAAA ACT GAATGACAAT ATGTCAACGT TAATTCCAAA AACGTAACTA TAAGTTACAA 300
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTATGGAGA GTTTGATCCT 360
 GGCTCAGGAT GAACGCTGGC GGCGTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420
 GCTTGCTTCT CTGATGTTAG CGGCGGACGG GTGAGTAACA CGTGGATAAC CTACCTATAA 480
 GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540
 CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600
 GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660
 CACTGGA ACT GAGACACGGT CCAGACTCCT ACGGGAGGCA GCAGTAGGGA ATCTTCCGCA 720
 ATGGGCGAAA GCCTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780
 CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAAGTGTGC ACATCTTGAC GGTACCTAAT 840
 CAGAAAGCCA CGGCTAATAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAACT GGAAACTTG AGTGCAGAAG AGGAAAGTGG 1020
 AATTCATGT GTAGCGGTGA AATGCGCAGA GATATGGAGG AACACCAGTG GCGAAGGCGA 1080
 5 CTTTCTGGTC TGTAAGTAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140
 CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCCTTAG 1200
 TGCTgGCAtA ACGCATTAAAG CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260
 10 AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

(2) INFORMATION FOR SEQ ID NO: 3195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60
 25 GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTCG TGCTAACAAT 120
 CGATGGTTTA CnAAACCTTA 140

(2) INFORMATION FOR SEQ ID NO: 3196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60
 40 GCATTTGTCG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120
 CTTTACCAAC GnTAATATTG TTGTC 145

(2) INFORMATION FOR SEQ ID NO: 3197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GTATGGGAAT 60
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCh 240
 CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300
 10 TnTTTCAGCTG 310

(2) INFORMATION FOR SEQ ID NO: 3198:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60
 25 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120
 AATTGAATCA GCTTTTnTCG 140

(2) INFORMATION FOR SEQ ID NO: 3199:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

40 TGGTGATTTC AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAAT TATTTTCGTTG 60
 TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTGTGTTAA 120
 AACCAGTGAT TGCAACCTGC CATTCAcAnG GAAAATTACC TAATAAGTGG CGTATTTACC 180
 45 AGTC 184

(2) INFORMATION FOR SEQ ID NO: 3200:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTGTC 120
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

(2) INFORMATION FOR SEQ ID NO: 3201:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

20 GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60
 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAGATA CGTAATGTnT 120
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

(2) INFORMATION FOR SEQ ID NO: 3202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

35 CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAACTGT 60
 AAAACGAGTG AATTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180
 AAAGTCCGAT TC 192

(2) INFORMATION FOR SEQ ID NO: 3203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTTGT ATTCGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAAGC 120
 ATCTTATAGC GTGATAGCCA TCGGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180
 5 TAAGCAGTAC ACACCAGTAA CATTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60
 20 TTTAATTACG nAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTTGTGC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TCGGCATTAT 60
 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACCTTCAGTG CTTACTGGnT 120
 CATCTAAATG ATTTTTAGCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60
 GACTTTCAGT CGTAACGTTT ACAAACCTTAA GCGCACGTCA nATGAAGCAT CGTGTAGACC 120

(2) INFORMATION FOR SEQ ID NO: 3207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60
 AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GntTAATGAA TGCATTAAGA 120
 AGCTGCAAGA ACTTATAAGT GTGCA 145

(2) INFORMATION FOR SEQ ID NO: 3208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnAAT CACACTTAGC 60
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTTATCAA CGGTATATGA AGGGGATTG 120
 GAAGATGCGT T 131

(2) INFORMATION FOR SEQ ID NO: 3209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60
 CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTCGTG AACAGCGCCA 120
 TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

(2) INFORMATION FOR SEQ ID NO: 3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60
10 AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120
AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

25 ATGCATACTG TATGTGTTCC AGCATATACA ATTTTGnCCA TCTTTAATGA CAACTGTACC 60
ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTTGATCTC 120
GGTAAAATTA ATTCTGC 137

30 (2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

40

ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60
AACAAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120
45 AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180
ATTTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT 239

(2) INFORMATION FOR SEQ ID NO: 3213:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

| | | |
|---|-------------------------------------------------------------------|-----|
| | CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG | 60 |
| 5 | TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT | 120 |
| | TCAAAAGTCT TGATATTTGA TACCCACGCT | 150 |

(2) INFORMATION FOR SEQ ID NO: 3214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

| | | |
|----|--------------------------------------------------------------------|-----|
| 20 | CTAAGCATTG GTTTAAACTA ATGTTTCAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT | 60 |
| | nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG | 120 |
| | TTACGATATT ATTAAACAAC TGTcTATCAT TAACGAAAGC AATTAACAAG AGTACTTGTT | 180 |
| 25 | GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC | 240 |
| | TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT | 300 |
| | TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA | 360 |
| 30 | TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC | 399 |

(2) INFORMATION FOR SEQ ID NO: 3215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

| | | |
|----|--------------------------------------------------------------------|-----|
| | CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG | 60 |
| 45 | CAGATAATTT AGATAAATAA TTAAACTTA GACATTCACC CAATCCTGAC AAAATATACT | 120 |
| | ATAACTAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr | 180 |
| | TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT | 240 |
| 50 | GACATCATTa AGAATATAAA TGC GTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA | 300 |
| | ATTTTTCAAT AACAAATTGCG CCACTAAAAC TCAAAATTTc CACCACCAAC ATCCAAATTA | 360 |

(2) INFORMATION FOR SEQ ID NO: 3216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120
 CTTGCTTTAT GCTATGGGTT TTTCAAACCTT AAA 153

(2) INFORMATION FOR SEQ ID NO: 3217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TG TAGACCCA TCAATTGCAG 60
 CCATTACATA TGC GGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120
 AnATAAAATT ATTACATC 138

(2) INFORMATION FOR SEQ ID NO: 3218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60
 TTATGCMTTT TaTTGCMcMA GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTCGATGGG CCAAACACAA 240
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTGA TTTAACAAAT TTATATGAAG 300

AACAACTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTC GAAACAATAT GGAGAAGCAG 420
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGCAGC 480
 5 ATATGCA 487

(2) INFORMATION FOR SEQ ID NO: 3219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

(2) INFORMATION FOR SEQ ID NO: 3220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTGC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCnGG 60
 35 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180
 40 TATGTAATTG TTTTGTGGTT ACG 203

(2) INFORMATION FOR SEQ ID NO: 3221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTTCAGA 60

GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240
 5 TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCCCTCA 300
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCCnGGGG TACACCTGGT CCACTTCATC 360
 A 361

(2) INFORMATION FOR SEQ ID NO: 3222:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120
 25 GTGCGTACAA GAATTAATCA AGGTTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60
 40 AATACATCTC CAACATTTGC CTThAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120
 TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCCCTAAGC ATATTTCTGA 120

TGATTTAACA CATTATGAAA CGAGA 145

5

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60

CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120

20

TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60

35

TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120

CATCTAnTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CAnAAATTCG TCATTCAGTT TCAACTTTAT 60

50

CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120

TTATCTGGCA ATAATCGTTG 140

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60
 TGACTTGCTT GATAAATAGC AACAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

(2) INFORMATION FOR SEQ ID NO: 3229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60
 ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GnTTCTACA 119

(2) INFORMATION FOR SEQ ID NO: 3230:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60
 CTAAATGTTG GAAAAATTTC TCCAGTCAAC AATGAAAGGC CATATGACTT TTCCTACAA 120
 GAGCAGGG 128

(2) INFORMATION FOR SEQ ID NO: 3231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60
 AAGTATCGTG TACAAGTTAT GAATGANTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120
 TTC 123

(2) INFORMATION FOR SEQ ID NO: 3232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC attCATATAG TTTGAAGTCT CGTTTAAAAC 60
 CATATCTATC ATTACGGTAT GCATATCTTT TAAACCTAT TCTTTTGTTA TTAGGACATA 120
 TAAATTCATC ATTAAGTTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180
 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT TTATTAAAAT 240
 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAAATAACC 300
 GAAGtATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360
 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420
 TTAAGTTGGC CATTTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480
 GTTTTAGAAA ArCTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540
 CTTTCGGAAT AATCATCAAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTtaCGGG 600
 TCTGTTTTCT AATTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720
 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTTGAAT 780
 TTTCGTTCAA TTTCGATTCTG TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840
 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900
 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020
 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080
 TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140
 CGCTATCAGG TATCGTTTCA ACAATTTTCAT TAACATATCG CGAAATATCA ATTTGAGGAA 1200

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500
 ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560
 10 CTGCTGTTTT TTTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTTTA ATAATTTGAA 1620
 TATGGrAAAT GTATTaWTct CTCATTTGTA TAGATT 1656

(2) INFORMATION FOR SEQ ID NO: 3233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

25 TTGCTCATAA ATCTTTTCTT GCGCTCTGA AACTATCTT CTATTCTGTC GGAATTTTTC 60
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120
 GGTAAATCCA 130

(2) INFORMATION FOR SEQ ID NO: 3234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

40 GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCCTGGG 60
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120
 45 AA 122

(2) INFORMATION FOR SEQ ID NO: 3235:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAACTG CTACTATTGA 60
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAGC ATTACATGCA TGAACCCAGT 120
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTTG CAGnTTCCAC ATG 173

10 (2) INFORMATION FOR SEQ ID NO: 3236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60
 AGCGATTAnA AAGCATTTAT CAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120
 CA 122

25 (2) INFORMATION FOR SEQ ID NO: 3237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

TTTTTTGCCC AAAATTTTTG GGTTTTTTTT GGGTTAAAGG AAAAAAATT TTAAAGGGG 60
 GGGGGGGGTC CCCCAAAAT TTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120
 40 CCCCCCCCCT TTGGAAAACC CCTTAAAAA ATTTAAAGGT TAAATTGGAA AAAAAAATT 180
 AA 182

45 (2) INFORMATION FOR SEQ ID NO: 3238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGAnGTTc GACAACGTAT TGTGGCAGAT GTTGcAGTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60
 GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60
 AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120
 AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60
 TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT 120
 GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60
10 TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60
25 GTTGTATATAG TCTAACAATG GTTGGCTCCT CTTtTTTTAT GTGCTAAAAA TTTATAGGCA 120
ATTTTATTAC AACAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATTT 180
30 AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60
CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120
45 ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

50

(2) INFORMATION FOR SEQ ID NO: 3245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

5 GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTAA AATTTGGAGA TTATGTGTGG 60
TGTTCAGTA TCGTTCA_nT AATTGATATT GCGCACCGT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAC TACGCACTGT GCCTTG_nTACA TACGCATGAT 60
20 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTTG_nCC AATTGTTACT ACCGTTC 117

(2) INFORMATION FOR SEQ ID NO: 3247:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACAnCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60
35 AGCCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60
50 ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120
CnTTTGGTCC TGCCA 135

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

10

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTACATG CCATCTGAAT CTCTAATTTT 60

AAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

25

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60

TCTAGTATTC CAAGTTGAAA AAACTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120

GA 122

30

(2) INFORMATION FOR SEQ ID NO: 3251:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

40

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60

CAAATTCATC AATCACAATT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120

45

CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60
 5 TGTAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

(2) INFORMATION FOR SEQ ID NO: 3253:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60
 20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120
 GTAACGGCAC TATATTGAAA 140

(2) INFORMATION FOR SEQ ID NO: 3254:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60
 35 TTTCTCTTCT ATTTAAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120
 CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC A_rACGTAGCA 180
 40 ATGAAATCAT CTAATTGTGC TTTAACCTWT TCTTGTGTAC CTGcAATGAT GCGTGCTTGg 240
 ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300
 TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACChA ATAACCAAAC ATCTAAGGCA 360
 45 GTTGTAAGCG GChACTTCCG CTTGTTATC AGChACAAG 399

(2) INFORMATION FOR SEQ ID NO: 3255:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTCGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAC 60
 5 GAAGCTATCG TCTCACTAnC CTTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAntTC AGTTAGTAAA 60
 20 AAGTCTGTGA GTAAGGGTGT ATGGAAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAAGTGT ACATCGTCTA ATAATAAGTT 60
 35 GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60
 50 GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAntTGGGAA AAGCCTT 117

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 124 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG 60
CACCTTGCAT ACTTTTTAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC 120
GnTT 124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

TACCAATGTA TATCCATATA CTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT 60
TTTGCTTGAT TAAATCTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG 120
TACAATAnAT 130

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCCTTAA TTTTTTAATT AAATTTTGGA 60
ATTAAAAAAG GAAAAAnTCC AAAGGTTAAT TTTAAAAAAA GCCCAAGGTT TTAAAAATTC 120
CCCCAACCAA AAAGGGGGGG AAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG 180
GGGCCCTCCC TTGGGGGTTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA 240
ATTGGGGGTT GGGGCCCTGG GGGAAAATTT TTGCCCTTTC CCAAGGGGTT TTTTAAACC 300
CGGATTTTTG GAAAAA AAAAGCCATTTT CCCCCCAACC CnAAAGCCCA GTTCCCGCCC 360
ATTTTCCCGG GGTAAACCCTG CCCCCACCGG GGCCATTTTT 400

50

(2) INFORMATION FOR SEQ ID NO: 3262:

55

(A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTTGGATGT TGAGAGACGT 60
 GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120
 GCGACGGCTG ATGG 134

15

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25

TTTTTTTCTG TTGGTACTTG TTTTGTGGTT GCGGATTGTG GTGTGTCTGA nTTAGTAGAT 60
 TGCATTGGTT GTGGCGTGTT TGCTTGATGG AGGTGTTGTC ACTTT 105

30

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40

GTTCCATCAT TCCCACcAT ATCCAACATG TGGGCTACTG CAATGCTTTA GCGTCAATG 60
 CCTCATCATC ATCACAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

(2) INFORMATION FOR SEQ ID NO: 3265:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

55

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTCGCCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

15

TTACCTTTAA AATAAnGTTT TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG

60

GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA

104

(2) INFORMATION FOR SEQ ID NO: 3267:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACAAACACAT GCAAATGGTT CAAGTATCAT

60

30

ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA

117

(2) INFORMATION FOR SEQ ID NO: 3268:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC

60

45

AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C

101

(2) INFORMATION FOR SEQ ID NO: 3269:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60
 5 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120
 ATTTATCCTA GGAAGCCGAT TAAAGGGTA CTGCCAGGGT TTTAGCCTGC nGCTGCCTCG 180
 GGGTTTTCTT TAAATTAATG nAACCGC 207

(2) INFORMATION FOR SEQ ID NO: 3270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

ATATTCGCAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTCAC AGTGATAAAA 60
 GGGCTTGGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

(2) INFORMATION FOR SEQ ID NO: 3271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60
 GATCAGCACC AGATATTGCA GGTA AAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120
 TT 122

(2) INFORMATION FOR SEQ ID NO: 3272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

GAAGGATGAT GATTCGGAGC AnCTTCTTGC AGAAGAnGCG GnaATAACGT GACATATTGT 60

TGCGAGCGCT TGACAATCTA TTCTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTGGA TTTTcTGAAA ATAAAGCAGT 240
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTTACTT TGTACATTAT TGTAATTTC 60
 GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTCGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60
 TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAActGGT AAGCCATTAC 120
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240
 nTGATGTCGC AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

(2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60

CCGGCGATAT CTGGCATCTT TTATTTTCGGC ATTTTTCCTAA ATCATGGTTA TTCCAGTTTG 120

5 GCGGCTTAAA AATTCnTT 138

(2) INFORMATION FOR SEQ ID NO: 3276:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60

20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

(2) INFORMATION FOR SEQ ID NO: 3277:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTTATC GTGTGGCATT 60

35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACCTGTT GCGAGTATTT CCGGTCTCGT 120

CATT 124

(2) INFORMATION FOR SEQ ID NO: 3278:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60

50 CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

(2) INFORMATION FOR SEQ ID NO: 3279:

55

(A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60
 GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60
 TTCGTTCCCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

40 ACTATGTTTG AnAAATTCTGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60
 ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

ACTTGGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

55

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

(2) INFORMATION FOR SEQ ID NO: 3283:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

15 AAATGACGAT AGAGTCAGGT ATTAATCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60
 TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

(2) INFORMATION FOR SEQ ID NO: 3284:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

30 TTAAGAAACC GAGCAGCGCA TAAncCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60
 CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

(2) INFORMATION FOR SEQ ID NO: 3285:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

45 TAAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAAC GGCTGTTTTA 60
 AAGCATCCTC CCATAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

(2) INFORMATION FOR SEQ ID NO: 3286:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60
 5 TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

(2) INFORMATION FOR SEQ ID NO: 3287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAATGCC TGGTAGAATA CTAATGAAAT 60
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCnAG AACCCATTTT TTGAATATTT 120
 CACCACTCGA ATCATCAATA C 141

(2) INFORMATION FOR SEQ ID NO: 3288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60
 35 GGCGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

(2) INFORMATION FOR SEQ ID NO: 3289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

(2) INFORMATION FOR SEQ ID NO: 3290:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTTT AAGCGATGAT TGCAATTAGA 60
 CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTATATT GGAGATGGTT AAAATGCTAA 60
 AACTCAACAT GAGTAACCAA AATATTGCCC TTAAAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

40 TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60
 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

55

GCGCGTAATA CCTGCAGTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

(2) INFORMATION FOR SEQ ID NO: 3294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT

60

AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n

111

(2) INFORMATION FOR SEQ ID NO: 3295:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTTGTCCG AATCCCCATC CTGCACCTGA

60

TAATAAGGCG AATAGCAAGT TGGTTCCCGT nGGGAAGCCA CTTGA

105

(2) INFORMATION FOR SEQ ID NO: 3296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTTGCCATG GCATGATAGT CCAGATACAT

60

GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTAAAAACCT GCGGGTTGGT TAAACCATTT

120

AACCTAAATG GGTTCCAAGG GTTAACGCGG TTAAATGTT TGGAAAGGTT TnCCCAGTTT

180

CCAAAAAGTT TTTnATTCCC C

201

(2) INFORMATION FOR SEQ ID NO: 3297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTCCTGA 60
 10 GAAATATTTT CATTCTTTAC ATTTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA 120
 TCTTGTAATT CTCTTGAAAC ATCATAATC TGGGCCACAT TTTCAGCACC TGAATCATT 180
 GATGGGTCGC TCATTTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT 240
 15 TCGTACACAG AATGCGGTCG TTTGATTTTC CAAGGTGCTC GACTTGTAAT TTCAACACCA 300
 CCTGCAATAT ATACCTTGCC AGCTCCGGCT TGGATCATGC GACATGCATA TTGAACACTT 360
 TCAAGTCCAG ACCCACATTG CCGATCGTT GTGACGCCAG TATTGAAGCT TAAGC 415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

30

TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC 60
 CCATTTAGGT GCATCGACCA ACTGCCCCGAC GAAAAGCCAT TTTGAAAACC AGAAGATGC 120
 35 CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG 164

(2) INFORMATION FOR SEQ ID NO: 3299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

45

GATAGTGCCA TTTTCACGTT TCTTAGTTAT TGGCATTTTT TAAATGCGAT GTGTGGCTTC 60
 TACATAACGG GAAATTTTAA GTTTTATGAA TCACATATC AATTGC 106

50

(2) INFORMATION FOR SEQ ID NO: 3300:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCANTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60
CATTTAAGGA AGCGATTCAC AATCGAGAAC ACAAAGTACA AC 102

10

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAATT GATATTGGCG 60
CACCGTATAA CCATGTCAAA GTACCATTG NAATCAGTCA TTGGCGCATT GGCTGCCCTA 120
GCGTTCA 127

25

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTTGAAACGT CCATGGACCC AATTGATTAA 60
TTGGnTGTA CTGGTCAAT GGGTATATCC TAAATGCACT GGCCTGCTGG TGTTCTTCTG 120
GGCGTTGCTT CGGAAAT 137

40

(2) INFORMATION FOR SEQ ID NO: 3303:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTCGATCT ACTTCCAGTC AATGCGTTTC 180
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATTATT 300
 TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTCGGTT 360
 10 AAAAGCGTTG GCACAATCCA CAATGCGAAC TGCCAAAGT 399

(2) INFORMATION FOR SEQ ID NO: 3304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

(2) INFORMATION FOR SEQ ID NO: 3305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAATGA CTCTAATGCC TTTTACCCA TTTTGTAAA TGGAACATGG 60
 AAGCATAGAG ATGCGTAGTC AGCTAGCGAC TTACCTTGAC GTTTTGCCTA TTCATTCCAG 120
 40 CTTTGTGGT ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180
 TTATGTCCAG TTGGACGCCA GA 202

(2) INFORMATION FOR SEQ ID NO: 3306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60
 AACTACTCCC G_nCAAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTCGTTA CCTGCGCCTT CTTTTGCGG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60
 35 ATGGTTCGCA ATAATTTTAA AATACCTTCC GCTACATTG ATTTAAAGCT GGTTGCGCAn 120
 TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCCCTTTTA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60
 50 GGA_nACGGAC ATTCAAAGG GATTTAGTTC ATCCAGATG GATTTCA_nTTT TGGGGAATTC 120
 CATTGGA 128

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCACCTACGA CATCTGTAGC TGGTATTGAT 60
CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60
CAGCGATTCCG GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60
AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120
TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60

GCACAGTTAA ATGATGCCAA AG 82

5

(2) INFORMATION FOR SEQ ID NO: 3314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60

TTATCAAAAT AGTGAGGGGC GTCATCA 87

20

(2) INFORMATION FOR SEQ ID NO: 3315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCATTT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60

TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120

35

TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGTnTA TTAGCAACTT GGAAGTGCCA 60

TTGTTAATTT CAGCTGTCTG TTACATTTCA ACCATAGTCT TTCACAAT 108

50

(2) INFORMATION FOR SEQ ID NO: 3317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT 60
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA 120
AAGATGATGC ATTAAATGCA CG 142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT 60
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA 120
AGAGCGAGTG ACTTAGGTCA AACAAACAGAG CAAGGCGAAT GGAAGCCAGT TATTCATGAT 180
GCAATCAGCG ATAGTTTAGT AGTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT 240
AAGAAGTGGA ACTTAAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA 300
ATGACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA 360
GATGGGATAT CATCGTCCAA TCChAC 386

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

ACAATGAATG ACATGATTCG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA 60
ATCGCCGGTC ATAATGTTTCG TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT 120
GGC 123

(2) INFORMATION FOR SEQ ID NO: 3320:

55

- (A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

10 GGCGAACTGT CAATTGCCGG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGTT 60
AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

25 GCGCCGGTTT TAACAGGTAA TTAAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60
AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

40 TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60
TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

55 TGCCAAATGT TCCCATAATT TCATTACGAn TCTTAAGTAG GTGGCTATCA TTACGATGCG 60

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCACTAAAA TAATAGTTGA 180
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300
 TAGTGCCAAA CGTTGTTTCA TACCCCCGGA cAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360
 TTCTAAATCA ACTAATTTAA GCTGTGCGTT AATCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGnATCC TAATGTATTT 60
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25 (2) INFORMATION FOR SEQ ID NO: 3325:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

35 TCTGAAnTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60
 TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40 (2) INFORMATION FOR SEQ ID NO: 3326:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

50 TGTCACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60
 TAGCCTTCTT CATTAACC 78

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60
ATATTCAC TA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCCGCGGT GGTTTCCGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60
CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60
TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

(2) INFORMATION FOR SEQ ID NO: 3331:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

15

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTTAA TAAACTCATA CCAAATCCTG

60

GGCATCTCTT

70

(2) INFORMATION FOR SEQ ID NO: 3332:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

30

CCTTGGGCAC CTTCAATTTG CATATTACGA CGTTTTCAG CTTGGTTCAA TTGGCAATAA

60

CTACACCTAG TGCAGTTGGA TC

82

(2) INFORMATION FOR SEQ ID NO: 3333:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

45

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA

60

AAAACAAGTA TATTGA

76

(2) INFORMATION FOR SEQ ID NO: 3334:

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTTCCTGGC 60

5 ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60

20 CATACGAGTA AGGG 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60

35 CATAGGAGAA AACAGG 76

(2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTTA CTAAAAAATG TATTTAAATA 60

AGTAGTACCT AA 72

50 (2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTTAATATGC 60

10 TGTCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

25 TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTTAATGAAT GTCTTCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

40 ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTTAATCCTT GGTGCTCTT TATTTTATTT AAATTGTAGA 60

55 ACCTAGA 67

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTTAC AAGCATCAAT CCATTAATTA ATAATTCCAT TAAATGTAGA 60
TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TGCGGATATC 60
ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGAAATGA 120
AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180
AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240
CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300
TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360
CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60
TCGCAGTGGT AATTTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

(A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10 CGGGAGGTGT TAAntCTTCA CAAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60
 TCGGTTTCAGG TGCCACAGGA AGTGATTCAG GTAGCnAAGG GTTATCTGAT ATTTTGAAAC 120
 CTGCATTAAAG TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180
 15 ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC 240
 CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTCG CGAAAAATTC GAAGAACACC 300
 ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360
 20 TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420
 TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAAACTGG AGAACGAATT TCTG 474

25 (2) INFORMATION FOR SEQ ID NO: 3346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35 AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60
 TTAG 64

40 (2) INFORMATION FOR SEQ ID NO: 3347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50 AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAAACAAAT 60
 GTTTTAAGTT GTTGATTTAA AATATTAAT 89

55 (2) INFORMATION FOR SEQ ID NO: 3348:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10 ATAACTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTCTCTT 60
AAAGAACAAT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT 107

(2) INFORMATION FOR SEQ ID NO: 3349:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25 CAACGCATCC TGCACCTTTTA CCTATTCCTG AATCACCGGT AATTAGTACA CCAACACCGT 60
AAACATCTAC TAAA 74

(2) INFORMATION FOR SEQ ID NO: 3350:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40 AGATGCACCT ACTTCTAACT GTCGCCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG 60
TA 62

(2) INFORMATION FOR SEQ ID NO: 3351:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55 GCTGCAAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT 60

(2) INFORMATION FOR SEQ ID NO: 3352:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTCGAT ATAGAACATC TAGCGACGTC GATTCGCAAG GTTGAACCAT 60

15 CTACATTAGG TGAGGAA 77

(2) INFORMATION FOR SEQ ID NO: 3353:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

30 (2) INFORMATION FOR SEQ ID NO: 3354:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

40 TTATGTAAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

(2) INFORMATION FOR SEQ ID NO: 3355:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATAACC TTTAGGGTTA CTACCAGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA 59

(2) INFORMATION FOR SEQ ID NO: 3357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCACGCCCTT TGAATATGGG AACTCAAAAC GATCTACTGG CTGATGTAAT 60

TACCCCTGTT TTGATTG 77

(2) INFORMATION FOR SEQ ID NO: 3358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA 59

(2) INFORMATION FOR SEQ ID NO: 3359:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA 59

(2) INFORMATION FOR SEQ ID NO: 3360:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25

GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTTGCTT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

40

(2) INFORMATION FOR SEQ ID NO: 3363:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50

CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTAA TCGTTGATT AAAAGTGGCA AAGCACGTGC ACATACGA 58

10

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

20

GTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT 58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTACTTT GTAATTTTCAAG TAACAGTTGA TCATCATG 58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC 58

(2) INFORMATION FOR SEQ ID NO: 3368:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

5 TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA 58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG 58

(2) INFORMATION FOR SEQ ID NO: 3370:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

30 CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA 60

TTGACGGC 68

(2) INFORMATION FOR SEQ ID NO: 3371:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

45 ATTACCAACA GCGAAAATAT TGAAAAGCTG TAAAAAAGCT GGTGCAsmCm TACTTGGATT 60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT 120

TGCACTTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG 180

50 CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA kCACTTTTAA CGACCAGTTA 240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT 300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA 360

(2) INFORMATION FOR SEQ ID NO: 3372:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA 58

(2) INFORMATION FOR SEQ ID NO: 3373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG 57

(2) INFORMATION FOR SEQ ID NO: 3374:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATTT CTTCGTG 57

(2) INFORMATION FOR SEQ ID NO: 3375:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA 60
 ACTAACAGAC 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG

57

(2) INFORMATION FOR SEQ ID NO: 3377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG

60

CTCGCATCCA

70

(2) INFORMATION FOR SEQ ID NO: 3378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT

56

(2) INFORMATION FOR SEQ ID NO: 3379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC

56

(2) INFORMATION FOR SEQ ID NO: 3380:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10 ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35 GAACACACAG GCAACCCAAA GCAGTGACGG CGAAAnTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

50 nGTATGTGAA AACTATTTGG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

25 TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTAAAT TATTTCTATT TGCTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

40 TCTTAACTGC A 71

(2) INFORMATION FOR SEQ ID NO: 3387:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

10 TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCAAC TTT TGTTCG 56

(2) INFORMATION FOR SEQ ID NO: 3389:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTTATTAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

35 AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

40

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

50 CAAACGCAAT AGCTGGTGAC TTAAGTGGG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTTATTAC AAAAGCCAAC TGTAT

55

10

(2) INFORMATION FOR SEQ ID NO: 3393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTG

55

(2) INFORMATION FOR SEQ ID NO: 3394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC

55

35

(2) INFORMATION FOR SEQ ID NO: 3395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCATT TGTTGGTACA GGTTATGGAA CACGTTGCAG CACGTGATTC TGGTGCGG

58

(2) INFORMATION FOR SEQ ID NO: 3396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

5

(2) INFORMATION FOR SEQ ID NO: 3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

15

TGTTGATGAG TCGTGTTTAA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

30

(2) INFORMATION FOR SEQ ID NO: 3399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

40

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

55

(2) INFORMATION FOR SEQ ID NO: 3401:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG 55

(2) INFORMATION FOR SEQ ID NO: 3402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG 54

(2) INFORMATION FOR SEQ ID NO: 3403:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT 58

(2) INFORMATION FOR SEQ ID NO: 3404:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT 60

TGTCT 65

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:

AAATTTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC 55

(2) INFORMATION FOR SEQ ID NO: 3406:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:

TCGATTTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC 56

(2) INFORMATION FOR SEQ ID NO: 3407:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:

AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT 60

TAAAGATTAG AAGG 74

(2) INFORMATION FOR SEQ ID NO: 3408:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

TGATTTTACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT 60

AGTGCTCA 68

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

(2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

(2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

(2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA

TCA

(2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10

ACTACCATTG CTTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC

53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC

60

TT

62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG

55

(2) INFORMATION FOR SEQ ID NO: 3416:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG

53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA 59

10

(2) INFORMATION FOR SEQ ID NO: 3418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20

CGTGGTCACC ATCACCAATT GCTCGATCTA ATTCAGTAAT TCAGATTCAT GTT 53

(2) INFORMATION FOR SEQ ID NO: 3419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT 55

35

(2) INFORMATION FOR SEQ ID NO: 3420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45

TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG 53

(2) INFORMATION FOR SEQ ID NO: 3421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

5 AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATAA TTAAAACTTA GACCATTAC 60
CCCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTAA ATGGACTCGC TAGATTAAAG TCGCAATAGT AGCGGCCGTT TCTT 54

20 (2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

30 CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

45 ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

(2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTC AAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

52

(2) INFORMATION FOR SEQ ID NO: 3427:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT

52

(2) INFORMATION FOR SEQ ID NO: 3428:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

52

(2) INFORMATION FOR SEQ ID NO: 3429:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAAGGT ATTATGGCGG CA

52

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTTCTTTTT TTATAAAAAT CTTATGCTTT 60
TTAACTAATT GTAAGA 76

(2) INFORMATION FOR SEQ ID NO: 3431:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGGTAAGTC GTATTAGAAC TAAAGCGGCT 60

(2) INFORMATION FOR SEQ ID NO: 3432:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

(2) INFORMATION FOR SEQ ID NO: 3433:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTAAATTT 60
TAAATTTTT 69

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:

10

GATCGCTATC CATTAGCTAA ATTTAAACGT TCAAACCTCAG GTACATGTTA C

51

(2) INFORMATION FOR SEQ ID NO: 3435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:

TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

51

25

(2) INFORMATION FOR SEQ ID NO: 3436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:

35

ATTAAAGCCA ACATTAATTT ATCCACTATT AACATAACG GCTACAGGCT TATTAATGAT

60

TTATACCTTT

70

40

(2) INFORMATION FOR SEQ ID NO: 3437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:

50

TTTGTGTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTCTTAG A

51

(2) INFORMATION FOR SEQ ID NO: 3438:

55

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10 GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G 51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A 51

(2) INFORMATION FOR SEQ ID NO: 3440:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35 CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA 55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAAACCAG TGTGTAAAAC CGGA ACTACT 60

50

ATGAGGGGCA TGAAAGT 77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGAATTAAA GCAAA

55

10

(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACTTTG GGATAAAGGT GATGCCCAA CTTTCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

45

ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC

50

(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

50

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTCCTCA TCTCTCTACT

60

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

TTATCACGGT ATATGAGGGG ATTTGAGG

88

(2) INFORMATION FOR SEQ ID NO: 3451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

(2) INFORMATION FOR SEQ ID NO: 3452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GCGGTGGATT ATCAAGTTTG

60

GGTA

64

(2) INFORMATION FOR SEQ ID NO: 3453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

AAGAATAAGT A

131

(2) INFORMATION FOR SEQ ID NO: 3454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGGA AGAAGCGCAn

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

(2) INFORMATION FOR SEQ ID NO: 3459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC

50

(2) INFORMATION FOR SEQ ID NO: 3460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG

60

CAAAAGCT

68

(2) INFORMATION FOR SEQ ID NO: 3461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

51

(2) INFORMATION FOR SEQ ID NO: 3462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

56

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:

10

ATACCAAATG TGAGAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT

50

- (2) INFORMATION FOR SEQ ID NO: 3464:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:

TCTTTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT

25

50

- (2) INFORMATION FOR SEQ ID NO: 3465:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:

AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTTG CCGACA

57

- (2) INFORMATION FOR SEQ ID NO: 3466:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:

ACATCCGAAA GATGACTTGT TTAAAAAAGC AGAGCATGAT TTGCTTACTA TGATTACACG

50

60

CGG

63

- (2) INFORMATION FOR SEQ ID NO: 3467:

55

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25

(2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

35

TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

50

CCCTGTTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

5 TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT 50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT 54

(2) INFORMATION FOR SEQ ID NO: 3473:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

30 TAATAGGCAT TCCATTAGG TCGTCGACA ACTGCAACGC AAGCATTGA AACAGA 56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA 55

45 (2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GGCGAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAATCATTCTG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGATGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG

50

(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTTCTG CTGCTAACGA GTTCCTGTGA CTGTTTCATGT CTATCACTTT GCGTTCCCTC

60

(2) INFORMATION FOR SEQ ID NO: 3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC

50

(2) INFORMATION FOR SEQ ID NO: 3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTCTGT TGTAGAACAA

60

GA

62

(2) INFORMATION FOR SEQ ID NO: 3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T

51

(2) INFORMATION FOR SEQ ID NO: 3483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT

54

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG

(2) INFORMATION FOR SEQ ID NO: 3485:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG

(2) INFORMATION FOR SEQ ID NO: 3486:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG

(2) INFORMATION FOR SEQ ID NO: 3487:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTGTGAT CACACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT
 AATGTAA

(2) INFORMATION FOR SEQ ID NO: 3488:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10

TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTTCG CCACCTTCAC CACTATATTT TCCCATGGTC

60

25

(2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

35

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC

50

(2) INFORMATION FOR SEQ ID NO: 3491:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT

52

50

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACCTCTTC TAATGGGATA ATCTCTTCAT GT

52

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACCGGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG 56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AACACGTA 59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT 55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

AntGTACACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA 50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

(2) INFORMATION FOR SEQ ID NO: 3501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

(2) INFORMATION FOR SEQ ID NO: 3502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

(2) INFORMATION FOR SEQ ID NO: 3503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GCGGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

(2) INFORMATION FOR SEQ ID NO: 3504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA

(2) INFORMATION FOR SEQ ID NO: 3506:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTTAAAA T

(2) INFORMATION FOR SEQ ID NO: 3507:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT
TTAA

(2) INFORMATION FOR SEQ ID NO: 3508:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT

(2) INFORMATION FOR SEQ ID NO: 3509:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

CAGATGCAAA TTGACATGGT CATCAACATC nGTnCATTAA AAGATGGACG

50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTCGATTCC CACCGCCACA TCATGATATT TATTCATAGA

60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG

94

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT AACTGAAAA ATGGGTAATG GTGCAAACAT AGTA

54

(2) INFORMATION FOR SEQ ID NO: 3512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn

50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC 58

10

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20

GTGTTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC 60

AATCTG 65

25

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35

ATGCCACTGA TAATGChnCT GAACTTATTG ATGACTTCTC ATTAGACTAT 50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC 50

50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTTC 50

20 (2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35 (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60
GTGATTTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

20 TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGA 57

(2) INFORMATION FOR SEQ ID NO: 3523:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

30 TGGTGGAGGT TTTGTTTTTT CCGTGTCGGT TTTTGTTTTT GTCTTGGTTT CTTTTGTTTT 60
TGTGTTCTCT TT 72

(2) INFORMATION FOR SEQ ID NO: 3524:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

45 ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC 59

(2) INFORMATION FOR SEQ ID NO: 3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGTACA 50

(2) INFORMATION FOR SEQ ID NO: 3527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT TGTATGCAGGC CT 52

(2) INFORMATION FOR SEQ ID NO: 3528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 3529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

5 (2) INFORMATION FOR SEQ ID NO: 3530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

30 GAATGCAAAA TCCATTGTGA AGGAnATCGA ATGGTTTAGT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

55

(2) INFORMATION FOR SEQ ID NO: 3534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGTCCA GTTTAATTTA CGAGTGGCGT AA 52

(2) INFORMATION FOR SEQ ID NO: 3535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60
 CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120
 ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180
 CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTTGTACAT GTTCGTGATG 240
 TAGATGGTGA AAAAAGTGA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAAC 300
 TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360
 TGCTTGGACA ACCTTCTTAT TTCCAATTC CAGAGGTTAT 400

(2) INFORMATION FOR SEQ ID NO: 3536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60
 GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120
 AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360
 5 CGTTTTCAAT ATTTTAAATG CTCATTTACA TAAGTAAACT CTGCTTTAAA ATAATTTAAC 420
 TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGA 480
 GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTA 540
 10 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCATT 660
 15 TACAAAAGTA AACTCCGCTT TAATTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTAAACCAA AAATATTTGA 780
 ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960
 TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGcGGT GTGTACAAGA 1020
 25 CCCGGGgACG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGcTCC AGCTTCATGT 1080
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

30 (2) INFORMATION FOR SEQ ID NO: 3537:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

40 GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAAmGTTG AAACATCAAC ATTAGGTGAA 120
 GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180
 45 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240
 TTACCATTCTG TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300
 50 ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360
 TATCTAAGAT ACTGGCGAnG ATTGTCACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420
 ACCC 424

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

| | |
|-------------------------------------------------------------------|-----|
| ATCTCATATG TTAAAAGGTA AACAAGGTCG TTTCCGTCAA AACTTACTTG GTAAACGTGT | 60 |
| TGACTATTCA GGACGTTTCA TTTTGCAGT AGGTCCAAGC TTGAAAATGT ACCAATGTGG | 120 |
| TTTACCAAAA GAAATGGCAC TTGAACTATT TAAACCATTC GTAATGAAAG AATTAGTTCA | 180 |
| ACGTGAAATT GCAACTAACA TTAATAATGC GAAGAGTAAA ATCGAACGTA TGGATGATGA | 240 |
| AGTTTGGGAC GTATTGGAAG AAGTAATTAG AGAACATCCT GTATTACTTA ACCGTGCACC | 300 |
| AACACTTCAT AGACTTGGTA TTCAAGCATT TGAACCAACT TTAGTTGAAA GGTCGTGCGA | 360 |
| TTCGTCTACA TCCACTTGTA ACAACAGCTT ATAACGCTGA | 400 |

(2) INFORMATION FOR SEQ ID NO: 3539:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

| | |
|-------------------------------------------------------------------|-----|
| AATAAGTAAG TTATTTTGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT TCCCATGCCG | 60 |
| AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC GCTAGAGTAG | 120 |
| AACGTTGCCA GGCAAATGAC AAATCGGAGA ATTAGCTCAG CTGGGAGAGC ATCTGCCTTA | 180 |
| CAAGCAGAGG GTCGGCGGTT CGAACCCGTC ATTCTCCACC ATTTATTCTT AGATATAGCC | 240 |
| GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT AGGTTGGGGG TTCAAGTCCT | 300 |
| CTGGCCGGCA CCATCTTTTG AGCCATTAGC TCAGCTGGTA GAGCATCTGA CTTTAAATCA | 360 |
| GAGGGTCAGA GGTTCGAATC CTCTATGGCT CATTACGATT TAATTTTAT ATTTAGCAAA | 420 |
| ATAATGCAGA AGTAGTTCAG CGGTAGAATA CAACCTTGCC AAGGTTGGGG TCGCGGGTTC | 480 |
| GAATCCCGTC TTCTGCTCCA TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC | 540 |
| TTAAAATCCT GCGGTGAGAG ATCACCGTAC CCGTTCGATT CCGGTCCTCG GCACCATTTT | 600 |
| AGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGAACGGA TCAAGAGGTT ATGGGTTCGA | 660 |

5 GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780
 TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840
 10 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900
 CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960
 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTATATG AGAGTTTGAT CCTGGCTCAG 1020
 GATGAACGCT GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080
 TCTCTGatGT TAGCGGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140
 15 GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

(2) INFORMATION FOR SEQ ID NO: 3540:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

25 CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60
 30 CTTAACGAGT ACCGGATTTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120
 GCACGCTTCG CCTATCCTAC TCGGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180
 GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240
 35 CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300
 GTCTTTCGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360
 TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCrC ACAGCTTCGG 420
 40 TaATATGTTT AGCCCCGGTA CATTTTCGGC GCAgTGTCAC TCGACTAGTG AGCTATTACG 480
 CACTCTTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGCnAC 540
 ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGnTTCC 600
 45 C 601

(2) INFORMATION FOR SEQ ID NO: 3541:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GCnAGGACCT TnCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCnC 60
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT 120
 TAAGTCCCCG CAACGAGCGC AACCCCTAAG CTTAGTTGCC ATCATTAAGT TGGGCACTCT 180
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300
 nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420
 TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTGT TCATTCAAAT 660
 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720
 25 CGAGTCCACT TAGGCCCACC ATTAATTTAA TACCTATTTG GGGGCTTAGC TCAGCTGGGA 780
 GAGCGCCTGC TTTGCACGCA GGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTATT 840
 30 TGTACATTGA AAAC TAGATA AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960
 CTCACAAGAT TAATAACGCG TTAAATCTT TTTATAAAAG AACGTAACCT CATGTTAACG 1020
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140
 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200
 40 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

(2) INFORMATION FOR SEQ ID NO: 3542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:

CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120
 CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180
 5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240
 GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300
 ACTTTTAATC AGAGGGTCAG AGGTTCGAAT CCTCTATGGC TCATTACGAT TTAATTTTTA 360
 10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAATAAC AGTTAATTAT ACCGGTGGTC GGGGTCGAAC 60
 25 CGCACTCCAC AAGTGGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120
 CTTAATGGTA AACAAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180
 CACCTATACC TCGTTCCGGG aAGGAACTGg TTcTAAAAGT TGAACTACTC CCGCAAATAT 240
 30 TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300
 CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360
 35 CCTATACCTC GTTCCGGGAA GGackTGTTt CTAAAAGTTG AACTACTCCC GCATAAACCT 420
 GGAGGCGGCA ACCGGATTG AACCGGTGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480
 TGGCTATGCg CcAATAACTG GGCTAGCTGG ATTCGAACCA ACGAGTGACG GATmAAAGTC 540
 40 CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600
 CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660
 GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720
 45 TGCCCCCTATT aAAAATaaTA ATkGGAGGGG GGCAGATTCTG AAntGCCGAA CCCGAAGGAG 780
 CGGGATTTAC ATTCCGCCGG GTTT 804

(2) INFORMATION FOR SEQ ID NO: 3544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240
 10 CATCGCATAA GTTTGATkAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360
 15 GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3545:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

25 CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60
 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120
 30 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCTTTT CGAACACGGA CCTTATCACC 300
 CATGTTCTGA CTCCAAGTT AAATTAATTG GcATTCCGAG TTTGTCTGAA TTCGGTAACC 360
 CGAGAGGGGC cCCTCGTCCA AAcAGTGGCT CTACCTCCA TAATCATCan TTGAGGCTAG 420
 40 CCCTAAAGCT AATTCGGAGA GAACCAGTAT CTCCAGTTCTG ATTGGAATTC TnCG 474

(2) INFORMATION FOR SEQ ID NO: 3546:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

55

GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120
 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180
 5 GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTCGTTCA CAGTGACATG 240
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GGCGCTTTGn GCGACACGGG 300
 TAAAAAAGC AGGCGAGTTC TATACACCAC AACAAGTATC TAAGATACTG GCGAGATTGT 360
 10 CACAGACGGT AAAGATAA_{nt} ACGTCACGTG TATGACCCAA 400

(2) INFORMATION FOR SEQ ID NO: 3547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TCGGCTCAT CGCATCCATT TTTGCCTGG 120
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTTCTTGA 180
 CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTGCGCTCT CGCTTACTCA TTTAGCTCTA 240
 30 CTAAACTCGT TCGGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC 300
 CATTTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAA AGAGACCTTG 360
 35 CGGTCTCAAT GCGGCTCATC GCATCCAnTT TTTGCCTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCCT AGGCGGTGGC TGTGAGCTTG 120
 50 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTTAC GTGATACAGA 360
TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60
AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA TTCCAGCTTC 120
ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180
CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240
GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300
AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360
CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60
TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120
TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180
TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240
AGGGTGATCG GCCACACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300
GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360
TCGGATCGTA AAACCTCTGTT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:

(A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA | 60 |
| | ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTAT | 120 |
| | TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TGCGAGCGCT TGACAATCTA | 180 |
| 15 | TTCTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC | 240 |
| | TTTTGTAAAT GAGCATTGTA TTTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA | 300 |
| | AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAAAATAT AGATTTTACC AAGCAAAACC | 360 |
| 20 | GAGTGAATAA AGAGTTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTCGAAA | 420 |
| | GAACACTCAC AAGATTAATA ACGCGTTTAA ATCTTTTTAT AAAAGAnAAC GTTTAGCAGA | 480 |
| 25 | CAATGAGTTA AATTATTTTA AAGCAG | 506 |

(2) INFORMATION FOR SEQ ID NO: 3552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

35

| | | |
|----|-------------------------------------------------------------------|-----|
| | AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT | 60 |
| | CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA | 120 |
| 40 | AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA | 180 |
| | GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA | 240 |
| | AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC | 300 |
| 45 | GAGCGAACTC TCGTTAAGGA ACTCGGCAAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC | 360 |
| | TCTTTAGGGT TAACGCCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA | 420 |
| 50 | AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG | 480 |
| | GAAGGTTAAG AGGAGTGGTT AGCTTCTGCG AAcTAcGaAT CGAAGCCCCA GTAAACGGCG | 540 |
| | GCCGTAACTA TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA | 600 |

55

5 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 720
 GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT 780
 AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC 840
 ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA 900
 10 AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATTG ATAGAGTGTA 960
 AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT 1020
 AGTGATCCGG TGGTTCCGCA TGAAGGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG 1080
 15 ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGCA CCTCGATGTC 1140
 GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 1200
 CGGTACrmGg CTGGGTTCAG AACGTCGTGA GaCAGTTCGG TCCCTATCCG TCGTGGGCGT 1260
 20 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 1320
 TACCAGTTGT CGTGCCAACG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA 1380
 AAcATnCTnA AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC 1440
 25 CCTCAAAGAT GATGAGGTTA ATAGGTTCGA GGTGGAAGCA TGGTGACATG TgGGAGCTGA 1500
 CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA 1560
 CTTACTATCT AGTTTTGAAT GTATAAATTA CATTATATG TCTGGTGAAT ATAGCAAGGA 1620
 30 GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG 1680
 AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTTGGTTAA 1740
 35 AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT 1800
 AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 1860
 TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT 1920
 40 CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA 1980
 CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG 2040
 AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA 2100
 45 CCGGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA 2160
 GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA 2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60
 AATAAGCTTG AATTCATAAG AAATAATCGC TAGTGTTTCA AAGAACACTC ACAAGATTAA 120
 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180
 10 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300
 15 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360
 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGAAGAGCC 420
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGACACTCT ATACGGAGTT ACaAAGGmCG 480
 20 ACATTtGACG AaTCATCTGG gAAAGwTGaT CCAAGGAA 518

(2) INFORMATION FOR SEQ ID NO: 3554:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

30 AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60
 CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120
 35 TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGGCAT GGAACAGGT GTGACCTCCT 180
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240
 40 AGTGATTTTG CTTGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420
 45 CACTTAeCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAA TTTCTACGC 540
 CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCCAGA 587

(2) INFORMATION FOR SEQ ID NO: 3555:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT 60
10 GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG 120
CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT 180
GAGTCGGAAT CACTGTCGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT 240
15 GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGg GTCAGAATCG 300
CTATCTGGAA TCTGGAGTCA CTGTCGGAAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT 360
ATCTGGAATC CGAnGTCATG GTCTGAGTCG GGaATCGCT 399

20

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT 60
ACAACCCCAA CAAGCAAGCT TGTGTTTGGT GGCTCTTCCC GTTTCGCTCG CCGCTACTAA 120
35 GGAATCGAA TTTTCTTTCT CTTCTCCGG GACTAAGAT GTTTCAGTTC TCCGGGTGTG 180
CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACATCATG CTGGGTTTCC 240
CCATTCGGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG 300
40 TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT 360
CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT 400

45

(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:

ACAACTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT 120
 CAAATTCCT ACGCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180
 CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT 240
 GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA 300
 AGCCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360
 CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420
 CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT GAGGGAACtT TGAGCGCCTC 480
 CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC 540
 ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600
 CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60
 TGGTATTACT GTTGCAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120
 GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCG 180
 CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240
 CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACTCTG 300
 AAAAAGTGGG TAATGGTGCA GAACATAGTA AGACAATTAA TGTGTTCGT GGTCAAATA 360
 ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACACACAT GGAAACGGCC 120
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATAACACGT 180
 5 AACACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300
 AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360
 10 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

(2) INFORMATION FOR SEQ ID NO: 3560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTTCCTAAGC GACCAATGTT 120
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCACCTATT TCATTAGTAT TCTTACCAGG 180
 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240
 30 TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTCCGT GTCGCAATTA 360
 35 GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TCGGATGATT 420
 GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480
 CGATT 485

(2) INFORMATION FOR SEQ ID NO: 3561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60
 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240
 AGGCATATGT TGTACCTATG ATGGTGAAG AGCCTTCAGT TGTCGCTGCA GCTAGTTATG 300
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAAACGGT ATCTTCTGAA CGTATTATGA 360
 TAGGTCAAAT CGTCTTTGAT GGC GTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420
 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463
 10

(2) INFORMATION FOR SEQ ID NO: 3562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60
 TTAATCTTGG TGCnGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120
 25 TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG 180
 TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240
 CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTT CTTAATGCAT TGTCTAACAA 300
 30 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360
 AAAAATATTT GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCg 420
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480
 TCCGATACGG CTACCTTGtT ACGACTTCAC CCCAATCATT TGTCCACCT TCGACGGCTA 540
 GCTCCTAAAA GGTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGCT GTGACGGGCG 600
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240
 5 TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360
 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3564:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAGCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60
 TAGTTGCCAT CATTAAAGTTG GGCACCTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120
 25 TGGGGATGAC GTCAAATCAT CATGCCCTT ATGATTTGGG CTACACACGT GCTACAATGG 180
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300
 30 ATGCTACGGT GAATACGTTT CCGGGTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360
 GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

35 (2) INFORMATION FOR SEQ ID NO: 3565:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

45 CAAACCATTG GTAGCTATTT GTAACCTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTGTA 120
 ATTCAATACA ATTGGTGTTG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180
 50 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAACG CTCATTGGTT 240
 TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

(2) INFORMATION FOR SEQ ID NO: 3566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CAcATTtAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60
 CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120
 CACCTATTGC ACGATTCGTT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGGTA 180
 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGTCACCTCAG CAATCTATCT GTTGAAGACA 240
 TTGATTTGAT CGAATTGAAC GAAGCATTtG CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTcATCCAT 360
 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTACtTAA TGAAATGGGT AGACGTCCCG 420

(2) INFORMATION FOR SEQ ID NO: 3567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTC 60
 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TATTATTTAC 180
 AAActATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTCATAC CCGTGAGGTC 240
 GGGGGTTCGA TCCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300
 TAGCTCAGTT GGTTAGAGCT AACGGCTCAT AACCGTTCGG TCGCAGGTTC GAGTCCTGCA 360
 GGTCCCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT 60
10 TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTT GCGATTCCGT 120
GTTTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA AGCAATAGAA 180
GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT 240
15 ACCGCAAAAA CAGTTGTCTC TGGAnTATAC ACACCTGATT GTTTTAATCC TTGTCTGACA 300
TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATTnA AAACCGCTTG ATGCGCCACC 360
ACAAGCCCCA CATTTCAAGT GATGGCATGG nTGTGGGTTn 400

20

(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA 60
GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG 120
35 CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG 180
ATTGGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC 240
GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC 300
40 TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA 360
TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC 400

40

45

(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

55

GTTTTATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120
 TTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180
 5 ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240
 CGACCGCCCC AGTCAAAGTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaA GyTAGCGCTC 360
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420
 AGTAAAGCTC CACGGGGTCT TTCCGTCCTG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540
 CG 542

(2) INFORMATION FOR SEQ ID NO: 3571:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATa 60
 aTaAAAATGT AATGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCh GCGTGACAGG 120
 CAGGCGTGTT AACCCCTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180
 35 CACCGGACTT CGGGTTATGA GCCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240
 AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC CCGTTAAGGc CCTGTCGGTT 300
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG GTAAATCGCT 360
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420
 CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480
 45 CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCaAG ACCGATCCCT TCAGCCGGAC 540
 TTGGGTATTc CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTKCGA CCGAACGGTT 600
 ATGAGCCGTT AGCTCTAAC 619

(2) INFORMATION FOR SEQ ID NO: 3572:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

5 GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60
 GCAGAATTAA TTGATCAAGC GGTTACTTCA TTGAGCCACA AGATTATTC AGTGCGATGA 120
 TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG 180
 10 TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240
 TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300
 AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360
 15 TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 3573:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

CAAATCGTAA CTCGCCGGTT CATTCTACAA AAGGCACGCC ATCACCCATT AACGGGCTCT 60
 30 GACTACTTGT AAGCACACGG TTTCAGGTTT TATTTCACTC CCCTTCCGGG GTGCTTTTCA 120
 CCTTTCCCTC ACGGTACTGG TTCACTATCG GTCACTAGAG AGTATTTAGC CTTAGGAGAT 180
 GGTCCTCCCA GATTCCGACG GAATTTACAG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240
 35 GAGACAACAT TTTCGACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC 300
 GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTTA CAACCCCAAC AAGCAAGCTT 360
 GTTGGTTTGG GGCTCTTCCC ATTTGCTCG CGGCTACTAA 400

40

(2) INFORMATION FOR SEQ ID NO: 3574:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1051 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60

55

TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240
 5 GTCGAACTTA CGTTCCGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAT CCACAGTAGC 300
 TCAGTGGTAG AGCTATCGGC TGTTAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360
 10 GCCATGGCTC cTtGGTCAAG CGGTTAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420
 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540
 15 GAATAAGCTG GAGGGGTAGC GAAgTGGCTA AACGCGGCGG ACTGTAAATC CGCTcCTTCG 600
 GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720
 20 GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840
 ACCAAATGTG GTGGGtATAT AATTAAAGA ACTATTTTAA AAATACAAC TTTAGAGCTT 900
 25 TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960
 CAAGCTGAAA ATCATCATTA TACGTGctTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATn 1020
 30 CACTTGATTA ATTnnATCTA TATAATGCCT C 1051

(2) INFORMATION FOR SEQ ID NO: 3575:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCGT 60
 CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120
 45 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT 180
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240
 50 AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360
 AATAgGTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAngTGAA 420

55

(2) INFORMATION FOR SEQ ID NO: 3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

TTTGTTCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG 60
 TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC 120
 GGGGCCCCAA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC 180
 CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAGGGCC 240
 CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC 300
 CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGCCCCAACA 360
 CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC 180
 TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA 240
 GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTCAC TGCGGCTCTT CTGGGCGTTA 300
 ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA 360
 GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC 400

(2) INFORMATION FOR SEQ ID NO: 3578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTTAG TTTAATGTT TGATGTGTTT CTGCTAAACC 60
AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120
TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAGA TGCAATGGTA 180
10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTC 240
AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300
GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGTCTTC GCAATCCACG GATATACCTT 360
15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3579:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG ATCGAACCGC 60
30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120
AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180
CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC CCATAACCTC 240
35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300
ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360
TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 400

40

(2) INFORMATION FOR SEQ ID NO: 3580:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

55

TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180
 AACAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240
 5 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360
 10 CCGTCTTCCA TGCGCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGGTACGGCT TTTCCAGAAG GATTACAAGG CCAAAACATT GCACGAACGA 60
 TTGCATTGCG TGCGGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180
 CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA 240
 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAGTCTG 300
 30 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120
 50 TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

ATTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGT

400

(2) INFORMATION FOR SEQ ID NO: 3583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC | 60 |
| | TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT | 120 |
| | ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT | 180 |
| 20 | CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA | 240 |
| | CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG | 300 |
| | CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAAACTCTCG TGGTGTGACG | 360 |
| 25 | GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ACTTATTGG CGATATTTTA AGTGATGAAG CTTCACTGAT TCCTGGTTCA CTTGGTTTAT | 60 |
| 40 | CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG | 120 |
| | CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTGGA AATGATTCTA TCTTTAGCGA | 180 |
| | TGTGTTTACG TGAAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT | 240 |
| 45 | ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG | 300 |
| | ATATTTTCGA AATTCTATCT CAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC | 360 |
| 50 | AAACATTATT TGACAANGTG TGGGACAGAC ATGTGTTATA | 400 |

(2) INFORMATION FOR SEQ ID NO: 3585:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC 60
TGTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG 120
TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG 180
ACCGATACCT GGC GTTGACC CTCTTGTCTT CGCAATCCAC GGATATACCT TAGTACCAGG 240
TAATTGACCA CCTTCACCAG GCTTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG 300
CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC 360
TTACTTTGGT GGCTTCCATC AACTTGTACT TCATAACGGT 400

20

(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC 60
TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG 120
AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA 180
CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACCTAT TGATGACTTA TCATTAGAAT 240
ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCGG 300
CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT 360
TATGGGTCCT GTAATTGATG TTCGATTTGA ACATAACGAG 400

40

(2) INFORMATION FOR SEQ ID NO: 3587:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

55

AGGATTCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATGGTG CCGAGGACCG 240
 GAATCGAACC GGTACGTGAT CACTCACCGC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300
 CCGCCACCCC GGCACATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTTCGC GACCTATTTT CTAATGCAGC 60
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180
 TAACTGGAAA GTCCTATTGA TGGATACTAG TAAACCATTA TTTAGTAAAT ACAGATGGAA 240
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAG 300
 ACGATATACT ACGACACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360
 35 GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCACCTAT AGATGGATCC 180
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360
 GTCTTCGGAT CGTAAAACTC TGTTATTAGG GAAGAACATA 400

5

(2) INFORMATION FOR SEQ ID NO: 3590:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CGGGTGAGAA TCCctCCACC GATTGACTAA 120
 20 GGTTTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACAg 180
 gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240
 GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300
 25 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360
 TCGAGTCGTT GATTTACACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480
 30 AAGGAACTCG GCAAAATGAC CCCGTAACT 509

(2) INFORMATION FOR SEQ ID NO: 3591:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 45 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GCGCTCTCC CAGCTGAGCT AAGCCCCCAA 180
 ATAGGTATTA AATTAATGGT GGGCCTAAGT GGA CTCGAAC CACCGACCTC ACGCTTATCA 240
 50 GCGGTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360

55

(2) INFORMATION FOR SEQ ID NO: 3592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACCTAA CATATATTTT GGGACCTTaG CTGGTGGTCT 60
 GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120
 AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTCTG GAGAGAACCA 240
 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300
 ACGTAAgTCG GTTCGGTCct CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360
 ATCACCTGGT TTCcGsGTst ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTCGC 420
 TAnGGCTCCA CATTACTGGn 440

(2) INFORMATION FOR SEQ ID NO: 3593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTC TTTATTCCAT 60
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAAC TTTCTGTGAA GTGTTAGGAA 120
 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180
 GTACAGGTTT TGGTTTATGG TCATTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240
 TTATnTACTA CCCATTCCCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300
 GTAAAGAAAG TAATTCAGAT TTAAAAGAAA AAGTTGCAGC AAACCTTTGA TACGAAAAAA 360
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

(2) INFORMATION FOR SEQ ID NO: 3594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
10 TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT 120
CCCCATTCCG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA 180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
15 TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT 300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATAA TTAACTCAT TGTCTGCTAA 360
ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAtTAATC CTCTCGCTC 409

20

(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT 60
GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTCAGCTGC TTCAAACAAT 120
35 ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TGCGCTTTTT CAATGCACTC 180
GTTGCAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAAC T 240
TCATTGCCT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC 300
40 CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG 360
GTAATTTC CA ATTTCGGCCTA GTTAATGGCA GCGGTTTTAA 400

45

(2) INFORMATION FOR SEQ ID NO: 3596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCTCCA 120
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180
 5 TCTGCTTGTA AGGCAGATGC TCTCCCAGCT GaGCTAATTC TCCAAAATAA TGACTCCTAC 240
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGcAACGTT CTACTCTAGC GGAACGTAAG 420
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540
 15 AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60
 30 TACCCAGCTA TGCCGTTGGC ACGACAACTG GTACACCAGA GGTATGTCCA TCCCGGTCCT 120
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180
 GTCTCACGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCCG GGTAGCTTTT ATCCGTTGAG 360
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240
 5 ATTTCTGTGTT GCTAAAACAA CAGCATGTAT GCCATTCATA ACACCTTTAT TATGTGTTGC 300
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATcGTTT GcaACCTCTT 360
 CTCCAGTTCT CTCGCCCCTT GGCTAAATCT TTAACAT 397

10 (2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCCTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC 120
 25 GTTGAGCGAT GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC 240
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300
 30 TCAAAGTGCC CGCCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

35 (2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120
 50 GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA

400

(2) INFORMATION FOR SEQ ID NO: 3601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

| | | |
|----|-------------------------------------------------------------------|----|
| 15 | ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG | 60 |
|----|-------------------------------------------------------------------|----|

| | | |
|--|-------------------------------------------------------------------|-----|
| | GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA | 120 |
|--|-------------------------------------------------------------------|-----|

| | | |
|--|-------------------------------------------------------------------|-----|
| | AGTAAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA | 180 |
|--|-------------------------------------------------------------------|-----|

| | | |
|----|--------------------------------------------------------------------|-----|
| 20 | ATTCATAAGA AATAATCGCT AGTGTTTCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA | 240 |
|----|--------------------------------------------------------------------|-----|

| | | |
|--|------------------------------------------------------------------|-----|
| | AATCTTTTTTA TAAAAGAACG TAACTTCATG TTAACGTTTG ACTTATAAAA ATGGTGGA | 300 |
|--|------------------------------------------------------------------|-----|

| | | |
|--|------------------------------------------------------------------|-----|
| | CATAGGTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG | 360 |
|--|------------------------------------------------------------------|-----|

| | | |
|----|---------------------------------------------|-----|
| 25 | GnCGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA | 400 |
|----|---------------------------------------------|-----|

(2) INFORMATION FOR SEQ ID NO: 3602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

| | | |
|--|-------------------------------------------------------------------|----|
| | GCTGTCTGAG TCGGAATCAC TGTnGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC | 60 |
|--|-------------------------------------------------------------------|----|

| | | |
|----|-------------------------------------------------------------------|-----|
| 40 | GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC | 120 |
|----|-------------------------------------------------------------------|-----|

| | | |
|--|-------------------------------------------------------------------|-----|
| | AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC | 180 |
|--|-------------------------------------------------------------------|-----|

| | | |
|--|-------------------------------------------------------------------|-----|
| | GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC | 240 |
|--|-------------------------------------------------------------------|-----|

| | | |
|----|-------------------------------------------------------------------|-----|
| 45 | TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC | 300 |
|----|-------------------------------------------------------------------|-----|

| | | |
|--|-------------------------------------------------------------------|-----|
| | TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT | 360 |
|--|-------------------------------------------------------------------|-----|

| | | |
|----|-----------------------------------------|-----|
| 50 | CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT | 396 |
|----|-----------------------------------------|-----|

(2) INFORMATION FOR SEQ ID NO: 3603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTCGCAATG AGATTGATGAT CGTnTTTGTC 60
CACTACAATA TCTAATAGTT TTAAGTTAAG TCCAGCATTG AAAAAAGTG CTGCCAGTTG 120
AGCGCCCATG GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC 180
AATTTAGTTG AGGATAAGAT AACCATTAAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA 240
ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT 300
TAAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG 360
AAAGCmGaAT CTCCAGTCaA AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT 420
TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT 480
AGTATGCCAT TACCACCTGT AATACGCGG CCCATAGCTA CnTCTCAC 529

25

(2) INFORMATION FOR SEQ ID NO: 3604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGG AAGCGATTGG TCGTCCTAAA 60
ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA 120
GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAAT TGTAATACG 180
TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA 240
GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA 300
CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA 360
TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG 399

45

(2) INFORMATION FOR SEQ ID NO: 3605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTCGATT 60
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT 120
 CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180
 10 CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC TCCCCTTCCG 360
 15 GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3606:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60
 TAAAAACATA TCGCCCCGTA GCTCAATTGG ATAGAGCGTT TGACTIONGGA TCAAGAGGTT 120
 30 ATGGGTTCGA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180
 ACTTGGTTTG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240
 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300
 35 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAATAA TAAGGCGGTG TAGCTCAGCT 360
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

40 (2) INFORMATION FOR SEQ ID NO: 3607:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60
 GTTTCCCATC CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

55

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCTTTTA 240
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTC TTCGAACACT AGCGATTATT 300
5 TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC GGTTTTGCTT GGTAATAATCT 360
ATATTTTACT TACTTATCTA GTTTnCAATG TACAAATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3608:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60
TGCAAAAGC CGCTCTCCCA GCTGAGCTAA GCCCCAAAT AGGTATTAAA TTAATGGTGG 120
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA 180
25 GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAC TGAATACAAT ATGTCACGTT 240
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGTC CCACCTTCGA 360
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCCGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3609:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAAATTCAAT CAGCAGAAGA ACTAGGACAT 60
45 GGCGCTTTTA AAATTATTGA AACACATGCA TTAAAAGATG TACAAGCAGT ATTGGGTTTT 120
CATAATGACC CATCGCGTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180
GCAGTAGATC GTTTTGAGTT TCATATTAAA GGCGTGGGTG GTCATGCTGC AAACCAGAAC 240
50 AATGCAACGA TCCAGTTATT GTGTTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360

(2) INFORMATION FOR SEQ ID NO: 3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
 TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT 300
 TAAATGCTCA TTTACATAAG TAAACTCTGC TTAAAATGA ATTTAACTCA TTGTCTGCTA 360
 AACGTTTTGC TTTTATAAAA AGATTTAAC GCGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC 60
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120
 GGCAACGTTT TACTCTAGCG GAANTAAAGT GNACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300
 TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC 360
 CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180
 10 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300
 15 GAGCCTCCGT TACCTTTTAG GAGGCGACCG CCCAGTCAA ACTGCCCGCC TGACACTGTC 360
 TCCCACCACG ATAAGTGTC GGGGGTTAGA AAGCCAACAC 400

(2) INFORMATION FOR SEQ ID NO: 3613:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240
 35 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300
 TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTTAT 360
 40 CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420
 TTATCAGGCG TGCGCTCTAA CCAGCTGAGC TATAGGcCCA TTTTTTTGaA TGTAAATAA 480
 ACATTCA 487

(2) INFORMATION FOR SEQ ID NO: 3614:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAT AATATGGTGG 60
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120
 5 CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360
 CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GChAGTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AACTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 AGATTCAAAC GTTTTCACCTT CGCCAAGCCA TTTTCTTTG TGTTCACCTT TTATTTTGAC 120
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300
 35 TCTTTTCTCG TTTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 360
 TTACTTTTTA TTTTGACGTT TAGGCATAAA AAAAAGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 3616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TnGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60
 ATTCACTCGG TTTTGCTTGG KAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120
 55 CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTAAACCAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGNATCCAG CCGCACCTTC CGATACGGCT 300
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360
 5 TTACTIONCACC GGCTTCGGGT GTTACAAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

(2) INFORMATION FOR SEQ ID NO: 3617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 60
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAT TTCTTTTATAG 120
 TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCGGAAT 240
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTTACGACT 300
 TCAnCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360
 30 TCGGGTGTTA CAAACTCTCG TGGTGTGACG GGCGGTGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60
 45 ATACTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTCGCAGA 120
 ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TAIGTTGTGT TTGCGCTTGT 180
 CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCAATTAG TACTAATTTG TGCAATGTTT 300
 GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA 60
 CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC 120
 TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180
 ACCCGTCTTT CGCTACTCAC ACCGGCATTG TCACTTCTAA GCGCTCCACA TGTCTTACG 240
 ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300
 CGGTAATATG TTTAGCCCCG GTACATTTTC GCGCAGTGT CACTCGACTA GTGAGCTATT 360
 ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

(2) INFORMATION FOR SEQ ID NO: 3620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60
 CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120
 GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180
 ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240
 AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300
 CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360
 CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

(2) INFORMATION FOR SEQ ID NO: 3621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240
 TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAACTGCC TGGCAACGTT CTACTCTAGC 300
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGT 475

(2) INFORMATION FOR SEQ ID NO: 3622:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60
 AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120
 CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGGCGTT 240
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAAACATT 300
 40 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360
 TTTAAGTCAG TCGCTAAAGA TTGTGGAAAG TAAGATCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3623:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CASACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTCCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300
 TGTATATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360
 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

(2) INFORMATION FOR SEQ ID NO: 3624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCTG AACCGCCGAC 60
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120
 25 GGCAACGTTT TACTCTAGCG GAAnTAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAGTGAT TTTGCTTCGC AACATTTAT 300
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTGTGACC TCTAACAGCA 60
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCCTCC TGATTCGTGT 180
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTACACC CATTCGTTTT 240
 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

(2) INFORMATION FOR SEQ ID NO: 3626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

15 GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60
 TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120
 AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180
 20 GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240
 TTCCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300
 TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360
 25 CCTATCTTCC GCTCCATAAT TTAATATTTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420
 CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

(2) INFORMATION FOR SEQ ID NO: 3627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

40 TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 60
 AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTCTTG ACTTGTGACA ATCGCTTGCT 120
 45 TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 180
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTGC 240
 TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300
 50 CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360
 GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3628:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60
 CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120
 ATTCCTACG ACCCACGACG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTTTG GGGGAGATAA 300
 GCCTGTTATC CCCGGGGTAG CTTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360
 20 CGGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

(2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTGAAAGG 60
 35 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTCATCTTC 240
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360
 45 CTnTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTTAAGTTGT nGATTTAAAA TATTAATAAA GTGTAAATTT GACTATTGAn ATTckrACaA 60
 ATACATATTA AAATAATATT TGTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120
 5 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240
 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTATG 300
 10 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATrATATTT 480
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

(2) INFORMATION FOR SEQ ID NO: 3631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAACTGAGC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGGC AATATGTAAG AATAAATGGT 120
 35 GGAGAATGAC GGGTTCGAAC CGCCGACCCT CTGCTTGTA GGCAGATGCT CTCCCAGCTG 180
 AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTCG 240
 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 300
 40 CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA 360
 AAAGTGATTT GCTTCGCAAA ACATTTATTT TGATTAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 180
 5 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAn GCCCCCAAnAT AGGTATTAAA 360
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

(2) INFORMATION FOR SEQ ID NO: 3633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60
 25 TGAGCTAATC AAACATCATA ATTTTATATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120
 GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACCTTCGG 240
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360
 35 CCAAGGCnAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

(2) INFORMATION FOR SEQ ID NO: 3634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA 60
 50 CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120
 TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTCGTCAGCT CCACATGTCA CCATGCTTCC 360

ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120

ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAA GAGACCTTGC 180

GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240

CGTAAGTTGG GCTACCATCG ACGCTAAGAA CCTTTCCTGA CTTGTGACAA TCGCTTGCTT 300

CTTTCCTCTT CTTGGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT 360

TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT ACTGATTTTC 60

AAAAAATCAA ATGCTCATT TACAAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120

TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180

TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240

ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300

GCACCTTTCG ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGTT CCACCTTCGA 360

CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

10 AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGGAATGTTA AATAAACATT 60
 CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180
 15 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240
 CGGGTGTTAC AACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300
 20 ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360
 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3638:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

35 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAGTAAGT CGAnCTACCA 60
 TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 180
 40 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360
 45 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

(2) INFORMATION FOR SEQ ID NO: 3639:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAAGCAGC GATAAAAATA 60
 ATCGCAATCG CTGGCAAACCT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCTGA TAGCGTTGTA TAGCCAACGA 180
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240
 ACAAATCTCC ATAAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420
 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480
 15 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAAGTC GTAATTCCT 540
 GATAGCCGGA T 551

20 (2) INFORMATION FOR SEQ ID NO: 3640:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

30 CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACCTGAT CCAACTTACA 60
 CTACCAATAG AACTTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120
 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180
 ICCTATCATC CAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240
 ICTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300
 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360
 TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3641:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGcAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240
 CTAAGCTGAG GCCGACAGnG TAqGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300
 AATCGTTTTA ATCGATGGGG GGrcGCATAG GATAGGCGAA CGTTGCGATT GGATTGCACG 360
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

(2) INFORMATION FOR SEQ ID NO: 3642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTA TAATCTTGTA 60
 25 CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180
 TTTCACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240
 30 ATGCGGCTGG CATTTCTGCT GCGACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360
 CAAAATGGka ATCATCGCCA TTAtTATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420
 35 TAATGACATT GCCTTCATG 439

(2) INFORMATION FOR SEQ ID NO: 3643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 50 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAA 180

GCGTGCGCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300
 CTGAATACAA TATGTCACGT TATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnC GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTCCGATCG TAAAACTCTG 60
 20 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240
 25 AACCGTGGAG GGTCATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

30 (2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATC 60
 TTTCTTTGTG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120
 45 CAATGCGGCT CATCGCATCC ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 180
 TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATnAT ACATTCAAAA CTAGATAGTA 300
 50 AGTAAAAGTG GATTTTGCTT CGCAAAACAT TTATTTTGA TTAAGTCTTC GATCGGATTA 360
 GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAAA GAGTTTAAAA 60
 TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAACAAGA TTAATAACGC 120
 GTTTAAATCT TTTTATAAAA GAACGTAAC TCAATGTTAA GTTTGACTTA TAAAAATGGT 180
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC CTTGGCACTA GAAGCCrATG 240
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300
 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420
 TCGATTCCCT TAGTAGCGGC GAGCANAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480
 GGGTnTGTA GACTCTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600
 TGaGTACGAC GGAGCACGTG AAATTCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660
 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720
 gGAAGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

(2) INFORMATION FOR SEQ ID NO: 3647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120
 AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTAAAG 180
 AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240
 ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

(2) INFORMATION FOR SEQ ID NO: 3648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

15 GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG 60
 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120
 TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180
 20 GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCTT TAGTGCTGCA GCTAACGCAT 240
 TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC 300
 CCGCACAAGC GgTGGaGCAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360
 25 TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCCT TCGGGGGACA AAGTGACAAG 420
 TGGTGCATGG TGTCGTCAAC TCCTGTCGTT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480
 GCACCCTTAA GCCTTAGTTT nCATCATTA GTTGGGCACT C 521

(2) INFORMATION FOR SEQ ID NO: 3649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60
 TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120
 45 ATACGTGTTT TAACACGTTC GTATCCCATT GCATCCCATA ATTGGAATGG ACCAAGTTTC 180
 CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240
 ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300
 50 TCGTCTTGcG CATTGAATAT GGTATCAAkG TTATGCACTA aGTCTTTATT AAATTCATTT 360
 AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:
GCCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTTCGAA CCCCCGCGGn CCGTTAAGGC 60
CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120
15 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180
TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG 240
AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT 300
20 TCAGCCGGAC TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTGCGA 360
CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

25 (2) INFORMATION FOR SEQ ID NO: 3651:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:
35 TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTTGCGCTA AATGCAACCA TGCATGGTAA 60
AAACTTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120
GTCCATTTAA TCATTTGACG ATTCACTTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180
40 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240
GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTTG AATGATTCAT ATATGATGGC 300
AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360
45 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:
(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

5 CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC 60
 GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120
 AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180
 TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240
 10 TCCCAAGTTA AATTAATTGG CATTCGGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300
 CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360
 ATTTCCGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

(2) INFORMATION FOR SEQ ID NO: 3653:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCGGTCC TCCATTCACT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60
 TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTTCG TACGGCTCCA 120
 30 CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTAC 240
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300
 35 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360
 CGTACTCAAG nATCCACTCA AGAGAGACAA CATTTTCGAC 400

40 (2) INFORMATION FOR SEQ ID NO: 3654:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

50 AAAGGTCCTA AATATAATTT TACAACTAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60
 CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

55

GCGCTCTCCC AGCTGAGCTA AGCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCGTA 300
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAA TCGATCAAAT CATCGATGAA GCGAAACATA 60
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120
 TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360
 30 GACCATGACG AAATTGTAAA AGCGAGTGGA ATTAACCAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480
 GGGTCTGGGG CTTGGGTTCC GGTTCCTGGGT CTGGGACTTG GGTTCCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60
 GTTGATCTGT CCCGATTTGT TGGTAAACGG TTGATTAATG AAAATGTTTCG CGAAGGGATT 120
 CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180
 GAAACAAATT ATCATTTCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240
 CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300
 ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360
 GGATTCATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60
 GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTGCGCTTG GAGTAATAAA 120
 AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180
 GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240
 GAATTTGGTG GTACTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300
 ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAAGAAA AACTTTCTCA ACAGCAAATT 360
 CmATTTCAAC AACGGAAAAA TCGCmACGTA TCTATATAAG GnGCGAACAG CTATGTGGTA 420
 ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCAGT 660
 5 AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60
 20 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120
 TGGTGGCAGG CTATATTTCA GGTGCTTGGG TTACGCAACT TATAACAGTA TTTAATGTCA 180
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240
 25 TTGGTGGCAG ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300
 CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAAnGTG 360
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCCAA CCTACTGATT 60
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120
 45 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180
 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240
 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300
 50 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA 360
 GTGATTTTGN TTTCGCAAAA CATTTATTTT GGATTAAGTC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

10 TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG 60
 GAATTAACGT TGACATATTG TCATTTCAGTT TTCAATGTTT ATTTTTCTTA CCGACAAGAA 120
 TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT 180
 15 TTTTAACCAA AATTGATTA AAAAAGTACC TGGCAACGTT CTACTCTAGC GGAACGTAAG 240
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 300
 20 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 360
 AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTTGAATG 60
 35 CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAA GCTTTTGTAT CAATTTTTTA 120
 TCGTCTTTTG TAATTTTCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT 180
 TGTAATTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG 240
 40 TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA 300
 ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA 360
 45 CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAAACTA 420
 ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG 480
 ATGACGTGTA CAAGCGCCGC ACGTTTTGCA GCGATTGAGC CGGCTAAACT AGCTAAGATA 540
 50 GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGATKGCTGC GTTTAAGCTA 600
 ATTAAATCTT GTTGATAAAA TTCTTGTAAG ATACCAATCG TCGCACTTGA ACTTTGAACT 660

AGCATTAAAT TGGCTTnAAA TC

742

(2) INFORMATION FOR SEQ ID NO: 3663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT | 60 |
| | TFTACTTACT TATCTAGTTT TCAATGTACA ATTTCTTTTT AGTCAAGCGC TCGCATACTG | 120 |
| | CTTTATTTTC AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT AATTTTTCTT | 180 |
| 20 | AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG | 240 |
| | CAATATCACT TTAACCAAAA AATATTTGAA TGTAAATAA ACATTCAAAA CTGAATACAA | 300 |
| | TATGTCACGT AATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG | 360 |
| 25 | GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

| | | |
|----|--------------------------------------------------------------------|-----|
| 40 | AACTAATAGT TCACTTTTAC TTTTTCTTT TTCATTATTA TCCATTATTT TTTCACCGCC | 60 |
| | AAAACGAATT TCATGATGTT AATTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT | 120 |
| | ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAKACATCAT TTAAAAGGAG | 180 |
| | CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AktGCTAGTA GTTGACTGAA | 240 |
| 45 | TGAAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCCAA CACAGAGAAT | 300 |
| | TTGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA CAGAGAATTT | 360 |
| | CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCAACACA GAGAATTTCTG | 420 |
| 50 | AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT | 480 |
| | CCCAaTTTCT ACAGACAATG CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC | 540 |

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

15 TATCATTTCC TGTTGCTAAA ACAACAGCAT GTATGCCATT CATAACACCT TTATTATGTG 60

TTGCTGCACG ATGAATATCT ACTTGGGCCA ATACAGAAGC ACGTTCCATT CGTTTGGCAA 120

CCTCTTCTCC AGTTCTCTCG CCCCTTGCTA AATCTTTAAC ATCAATTTTCG CCTTGAACCT 180

20 TAACAACGGA CGCTGTTGCA TGATTGGATA AAATACTCAT TAAAATGTCG CTTTGGGAAA 240

tTCATTTTTT AAAAATGCAG TTATGGCCTC TAAAATCGTA TTAAGCATAT TAGCGCCCAT 300

AGCATCTTTC GTATCAACAA ATACTTTTAA AGATAGTAAC TGtTGcTCAG GrAATGTakC 360

25 mAtCGCTATA CGtTGGTAAC CACCACCACG CGCTTTAATA GGAA 404

(2) INFORMATION FOR SEQ ID NO: 3666:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCCAG TAGCAATTAT TGAACGATAT TAGGCTATCT AGTCGGCATA TTTGTAAAAC 60

AAGATCCAAT TAAATATCAA CAGGAATAAC GAATAATATA AAAGAGGTTG GGACATAAAT 120

40 CCCTAAAAAA ACAGCAGTAA GATAATTTTC AATTAGAAAA TATCTTACTG CTGTTCTCTA 180

TTTATACAAT ACTTCGTATT GAATGGCTTC GCTTTCCTAG GGTGCCGTCT CAGCCTCGGT 240

45 CTTGACTGG CACTGCTCCC TCAGGAGTCT CGCCATTAAT ACTACGTATT AACGTGTAAT 300

TTTACTTTGA AATACTTTAA AAAAATAAGA CACTTTGCCC AACTTGCACA TAAATGTAAA 360

ATTCAATAAA ATAAATTCTT GTGTTGGATC CCTnCGTATA 400

50

(2) INFORMATION FOR SEQ ID NO: 3667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

| | | |
|----|--------------------------------------------------------------------|-----|
| | CCAACAAATC TGTCTGTCGC ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC | 60 |
| 10 | CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA | 120 |
| | ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC | 180 |
| | CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG | 240 |
| 15 | GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA | 300 |
| | CCTTTTAAAG TATTACGTAA TGTGTGTGTTG CGGTTTACAT CTTACCCAAA GTGCTAATGC | 360 |
| 20 | GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT | 60 |
| | AACATGACAT AACTCATGAC TGGGTTTCCC CATTCGGAAA TCTCTGGATC AAAGCTTACT | 120 |
| 35 | TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG | 180 |
| | CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT | 240 |
| 40 | TAATCTTGTG AGTGTTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT | 300 |
| | AAAACCTCTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT | 360 |
| | TTTCAATGTA CAATTTCTTT TTAGTCAAGC GCTCGCATAA | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTCGC 180
 5 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCTATA 240
 GAGTGTAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCAn GGTCGAAAGA 300
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360
 CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

(2) INFORMATION FOR SEQ ID NO: 3670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATCTTTC 60
 25 TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120
 GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTCG 180
 30 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 240
 CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT CTTCCGATCG ATTAGTATTC 360
 35 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCCGAACCT 400

(2) INFORMATION FOR SEQ ID NO: 3671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60
 50 TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120
 AAATTTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180
 TAAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACCnA nAGGnAGAAT 360
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCG AGAAAGAACG 60
 TAAATTTAAT cCTGATTTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120
 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300
 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAGGA GACTCGATTG TAGAAAAAGA 420
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA 60
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120
 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCCAGC TGAGCTAAGC CCCCAAnAG 180
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240
 TGCGCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAACTG 300
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTTCCGAAT ATATCCTTAG 360
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA 60
 GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT 120
 ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT 180
 ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA 240
 TCAGTAAGTA AACAGTGGTG GGTTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA 300
 TTGGAGGATG GAAATGATT ATGTACGCCA TTAACGTCAA ATTCTTTTGG CGTAAATGTC 360
 TTTGTACCAA GTCAACAATC ATATACCAGT AGTCCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC 60
 CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACCTGCCTG 120
 GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300
 TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT 360
 CGGACCTATT AACCTCATCA ACCTTGAGGG nTCTTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 3676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

5 TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60
 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180
 GCCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCCTGT ACCACCTATA ATCGTTTAA 240
 10 TCGATGGGGG GACGCATAGG ATAnGCGAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3677:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60
 TATTTTCTT CTACTTTTGT TTTTCTGCG GCAATTGTT GGTGAGTCGC ATCACCATTG 120
 30 TTAATAACAT TTTGTGCATT TGTGATTCT GTTGACCCG CACGTTTAGC ATTTTCATAT 180
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAAT 300
 TGCTTGCGTT AATCGCTCAT TGACACGATT TACATTGTT AACGCAGATT GCACTTCTTG 360
 TACTGTTCTT AATGGGCTTT TGAATAATA GCATTAGCGC 400

40 (2) INFORMATION FOR SEQ ID NO: 3678:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 648 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

ACAGTCAATT GnTCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

55

AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAAATATT GCGGGAGGCG GATTTGAACC 240
 ACCGTACTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300
 5 AAATAATGGC GGAGGAAGAG GGATTCGAAC CCCC GCGGCC CGTTAAGGCC tGTCGGTTTT 360
 CAAGACCGAT CCCTTCAGCC GGAATTGGGT ATTCCTCCAT TATTATAGGT AAATCGCTAT 420
 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480
 10 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540
 ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

(2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60
 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120
 30 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTCCGAT GACAGCTTCT 180
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTTGTGC AATTCAAACG TGTACTTTCC 300
 ACCGTTTTTC ATTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360
 TTCAATAAGT TGTTTTCTCA ATTTAAAATC AAGTTCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTCTTGT CTAGCAACGT TCTACTCTAG CGGAAnTAAG 60
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGAATTGTGA CAATCGCTTG CTTCTTTCCT 120

TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300
 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360
 CGCTTGGCTT CTnTCCTCTC CTTCGGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 60
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCCAAG CCATTTTTCT TTGTGTTTAC 120
 TTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180
 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300
 AAACGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

TTGAACATGT TGAATCTAAT GAAATTCTTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTGAGTAT AACGAGATTT 180
 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240
 TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

(2) INFORMATION FOR SEQ ID NO: 3683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

TTGGAATTC TCCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTCGGT 60
 CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT 120
 CTACGACCAA ATACTAAACG CCCTATTCAG ACTCGCTTTC GCTACGGCTC CACATTTACT 180
 GCTTAACCTT GCATCAAATC GTAACGCGC GGTTCATTCT ACAAAGGCA CGCCATCACC 240
 CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCTTC 300
 CGGGGTGCTT TTCACCTTTC CTCACGGTA CTGGGTTTAC TATCGGTCAC TANGAGAGTA 360
 TTTAAGCCTT ANGAGATGGT CCTCCAGAT TCCCGACGGG 400

(2) INFORMATION FOR SEQ ID NO: 3684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

GATnTATGAT GAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT 60
 TCACTTATAC TTCTAGTCAC AGATThAAAT AATCAAAAGT GCACATTATT AAAATATCAA 120
 TTTCACACTC AATGCGGCTC ATCGCATTCA TTCTTTGTCT AGCAACGTTT TACTCTAGCG 180
 GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTcTT GACTTgTGAC AATCGCTTGC 240
 TTCCTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC GTTGCGCTCT 300
 TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT TTTGTGTTTA 360
 CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG 420
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA 480
 CTTGTGACAA TCGCTTGCTT CTnTCCTCTC CTTCGGCTCT CGGTACT 528

(2) INFORMATION FOR SEQ ID NO: 3685:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

10 AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180
 15 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240
 TTCAGTGCGA TGATTCGTGA AATTGAAACG CAAGATTTTCG ATATAGAGCA TCTAGCGACG 300
 GCGATTCGCA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360
 20 CTGTTCAACG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3686:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCACT CTTCGGTGGT 60
 35 GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240
 40 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360
 45 GATTTTAAAT TATTgAAAAT AAACCATATA CAGGTGCAAC GGT 403

(2) INFORMATION FOR SEQ ID NO: 3687:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCCGCGAT AATAAAAAAT AATGGCGGAG 60
 GAAGAGGGAT TCGAACCCCC GCGGCCCGTT AAGGnCTGT CGGTTTTCAA GACCGATCCC 120
 5 TTCAGCCGGA CTTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240
 ACCGCTACAC TACGAGACCA TTAGTAAAC GGAGGAAGAG GGATTCGAAC CCCC GCGAGC 300
 10 CGTTAAGCCC CTGTGCGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360
 AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTATGAGC CGTAGCnCTA 420
 ACCACTGGGC TAAAGTCCTA ATATAATTT 449

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TCnATAATGC 60
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120
 30 TGCTTACGGT GCATTACACG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCC 180
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240
 TGAATTAGAT TGTGACATTT TAGTACCAGC GGCTATTTC AACC AAATTA CAGAAGACAA 300
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAT TTGAATGAAC 60
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTC 120

CGACTTCACC CCAATCATTG GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240
 CGGCTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360
 TGCAGACTAC AATCCGAAC T GAGAACTT TATGGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 3690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 553 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

GCnGCGTTTT AGGCCCATTC GGTTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60
 TGAACCCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180
 25 CAACTGAGCT ACTGAACCAT AATAAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300
 TTGCGGGAGG CGGATTTGAA CCACCGaCT CGGGTTATGA GCCCGACGAG CTACCGAACT 360
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC 420
 CCGTTAAGGC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480
 ATTATTATAG GTAnATCGCT ATTAATTATA AnATTAAAT GGCGGTCTCG ACGGGAATCG 540
 35 AACCCGCGGA TCT 553

(2) INFORMATION FOR SEQ ID NO: 3691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 120
 TCTTCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300
 ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG ATTGAGTATA 60
 20 TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAACA TATCGCGAAA 180
 TATCATTTTG AGAATTCTAA CGAATTTCTT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240
 25 ATTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60
 TTTTATTTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACAAATGC 120
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTTCCTAG ATTGTGCTTT 180
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCa ATAACAGGTG TTACTACTTT 240
 ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300
 50 ACCAGGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTTGGT GTTCCGGCT CGCTTGGTAC 360
 TTCTGGTGTC GGTGGTGTG GGTGTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCGGT 420

(2) INFORMATION FOR SEQ ID NO: 3694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60
 ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120
 ATTAGCTACG GTTTCCTCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCAATG 240
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360
 AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCCTGTGC 60
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAT GGTCTTTTAA 180
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240
 CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC 300
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360
 TTGGTATAAC TTAATTTCTn CTTTTCTTC ATCnGGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240
 CATTTTTATA AGTCAAACGC TCACATACGG CTTCGTTTTC ATTATTTTAA ATGCTCATTT 300
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360
 15 TAAAAAGATT TAAACGCGTT GATTAA_nCTG TGAGTGTCTT 400

(2) INFORMATION FOR SEQ ID NO: 3697:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240
 35 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300
 TTACTA_nCGA TTCCA_nCTTC ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA 360
 CTTTATGGGA TTTGCTTGAC CTCGCGGTTT CGCT_nCCCTT 400

(2) INFORMATION FOR SEQ ID NO: 3698:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

50 AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

55

CCCCATTTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAAAGCA TATCGTCGTT 180
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240
 5 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTGGAACAC 300
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAAACTC TTTATTCACT CGGTTGTGCT 360
 TGGnAAAATC TATATTTTAC TTAATTATCT AGGTTTCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3699:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCGT TTGCAAATCC 60
 AAATTCTTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACCTACC 120
 25 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTTG GTGAAGCCCC 240
 TGTAnCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA 300
 30 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360
 CGCATTTTTT AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3700:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCGTGTGT TCGGCATGGG AACAGGTGTG 60
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120
 TAAGTAAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180
 50 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT 240
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnC GGGGGGCTTC ATGCTTAGAT 300

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

(2) INFORMATION FOR SEQ ID NO: 3701:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

15 AACCAAGCCC AATAATGGAC TGGCCGCCTA ATAATAAAAG CTCTAAAAGT TGTATTTTAA 60
AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT 120
CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180
20 TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC 240
GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300
TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGnTT TACAGTCCGC 360
25 CGCGTTTAGC CAnTTCGnTA CCCCTCCAGn TTATTCATAT 400

(2) INFORMATION FOR SEQ ID NO: 3702:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

35 TTTAAGTCCT GTGCGTCTGC CAGTTCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60
CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAACCTACTT 120
40 CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180
TGCGTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240
45 ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300
CGGCCAGAGG ACTTGGAACC CCCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360
GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

50 (2) INFORMATION FOR SEQ ID NO: 3703:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
- 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT 60
10 ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAACT 120
AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGGc GCTCTCCCAG CTGAGCTAAG 180
CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 240
15 CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG 300
TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG 360
CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG 400

20

(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACCAATTATT ACGTCAGCTT 60
ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG 120
35 TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTCAG 180
CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA 240
GCACTCGCGG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT 300
40 AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAAA GGTAACACTA 360
TCATTTATGC AATACGGCGC ATTACCCAGA GTTGCATGGT 400

45

(2) INFORMATION FOR SEQ ID NO: 3705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

55

5 TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180
 AAAGTGACAG GTGGTGCATG GTTGTCGTCA GCTCGTGTCG TGAGATGTTG GGTTAAGTCC 240
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300
 10 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAAA TCATCATGCC CCTTATGATT 360
 TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

15 (2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60
 TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTCGCGA 120
 30 TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCCAAAAAGG TCATGCTGAA ACGTTGAAAn 300
 35 CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360
 AAGCAGTAGA AGATGTTCCA TAACTTTGG TGAGGACCCT 400

40 (2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

50 GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAATCGAA CCCGCGATCT CCTGCGTGAC 120
 AGGCAGGCGT GTTAACCGCT ACACTACGAG ACCTATAAAA TATTGCGGGA GCGGATTTG 180

55

TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCG 300
 GTTTTCAAGA CCGATCCCTT CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC 360
 5 GCTATTAATT ATAAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCAT TAAAGCGGTA CCAngCTGGG TTCAGAACGT CGTGAGCAnG TTCGGTCCCT 60
 20 ATCnGGGGTG GGCCTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120
 GACATACCTC TGGTGTACCA GTTGTCGTGC CAACGGCATA GCTGGGTAGC TATGTGTGGA 180
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCCTC AAGATGAGAT TTCCCAACTT 240
 25 CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360
 30 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAAT ACTATTAAGA AGTCCTGAAA 60
 AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120
 45 CAGTGTTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTTGTTCT 180
 TGCAACGCTA TTTAGTATCA GGTTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATTx 240
 50 GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360
 CCAAGTTTAC AAAAAGTTGA AAATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTCGAA 420

(2) INFORMATION FOR SEQ ID NO: 3710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

| | | |
|----|--------------------------------------------------------------------|-----|
| 5 | AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC | 60 |
| 10 | | |
| 15 | CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT | 120 |
| 20 | TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT | 180 |
| 25 | TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA | 240 |
| 30 | CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC | 300 |
| 35 | TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG | 360 |
| 40 | TGCGTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG | 420 |
| 45 | ACCCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG | 480 |
| 50 | GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT | 540 |
| 55 | AACCAATTG AGCTAAGGC | 559 |

(2) INFORMATION FOR SEQ ID NO: 3711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

| | | |
|----|--------------------------------------------------------------------|-----|
| 40 | AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG | 60 |
| 45 | GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC | 120 |
| 50 | TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTTCATT | 180 |
| 55 | CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCTGATAAGC GTGAGGTCGG | 240 |
| 60 | TGGTTCGAGT CCACTTAGGC CCACCATTAA TTAAATACCT ATTTGGGGGC TTAGCTCAGC | 300 |
| 65 | TGGGAGAGCG CTGCTTTTGC ACGCAGGAGG TCAGCGGTTT GATCCCGCTA GTCTCCACCA | 360 |
| 70 | TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT | 400 |

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

| | |
|-------------------------------------------------------------------|-----|
| TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG | 60 |
| CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA | 120 |
| CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA | 180 |
| AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATTCCAA TCGAACCTGG AAATAGCTGG | 240 |
| TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT | 300 |
| GTTTGGACGA GGGGCCCTC TCGGGTTACC GAATTCAGAC AAACCTCCGAA TGCCAATTTA | 360 |
| ATTTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

| | |
|--------------------------------------------------------------------|-----|
| TTTTTAAGTC TGATGTGAAA GCCCACGGCT CAACCGTGAA GGGTCATTGG AAACCTGGAAA | 60 |
| ACTTGAGTGC AGAAGAGGAA AGTGGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT | 120 |
| GGAGGAACAC CAGTGGCGAA GCGGACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC | 180 |
| GTGGGGATCA nACAGGATTA GATACCCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG | 240 |
| TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGTAAACGCA TTnAAGCACT CCGnCTGGGG | 300 |
| AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG | 360 |
| AGCATGTGGT TTAATTTCTGA AGCAACGGAG AGGAACCTGA | 400 |

(2) INFORMATION FOR SEQ ID NO: 3714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAA_nT CGACTACCAT 120
 CGACGCTAAG GAGCTTAACT TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180
 10 AGTCACCAGA CATATGAATG TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT 240
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300
 cAtGTCACCA TGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360
 15 CCGAAGTTGG GAAATCTCAT CTTGAGGGGG GCTTCATGTC TTAGCATTTT AGTCACTTAT 420
 GCCCCG 425

(2) INFORMATION FOR SEQ ID NO: 3715:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTGTAGG TTTGTCATGC 60
 CCAGTTACAA GTTGCGTTAT CGTAGACACT AACATTAATA TGA_nCTGGTAA TGTGCTGTT 120
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTT_nTG TGCACCTAAC 180
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTT_nTGTC ACTTTGTTAA 240
 ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA GTAATACATC 300
 TCCAACATTT GCCTTTAATT CTTT_nTGCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT A_nGTAGTCCT 400

(2) INFORMATION FOR SEQ ID NO: 3716:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT 60

GCAATATCAC TTAAACCAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180
 ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240
 5 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300
 TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC GGnTTCGGGT GTTACAAACT 360
 10 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60
 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120
 25 GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180
 TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAnGAGTTGA AATAGAACCT GAAACCGTGT 240
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300
 CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA GCCGTAGCAn AAnnTGTTCT 360
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 3718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60
 AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120
 50 AGGCTCATAA AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240
 GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAAATAAGT 300

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGTnA

400

(2) INFORMATION FOR SEQ ID NO: 3719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | ATTTAAACT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA AGTnGAGCTA CCATCGACGC | 60 |
| | TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC | 120 |
| | CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT | 180 |
| 20 | TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT | 240 |
| | CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA | 300 |
| 25 | GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT | 360 |
| | CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAngG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

| | | |
|----|-------------------------------------------------------------------|-----|
| 40 | CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT | 60 |
| | TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC | 120 |
| | TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA | 180 |
| 45 | AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG | 240 |
| | TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT | 300 |
| | CACAATTTCA TTTTGCGTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA | 360 |
| 50 | CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG 60
GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT 120
GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC 180
AGCCGAAAAT GGATGGTGTG AAGAGCGTTA CTTGGTTTGG CGGTATGCTT ATTTTAAATG 240
GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG 300
TGGTGTGTT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GGCGCCACTG AnAGATCGTG 360
GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCAGCGCA 400

20

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA 60
TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT 120
GGATTCGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT 180
TAATAATAAG GGCGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT 240
GTTAACCCTT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG 300
GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCCCTA TTAAAATGAT AAATGGAGGG 360
GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC 400

40

45

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

55

GGTTCAAGTC CTCTGGCCGG CACCATTtTtT GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTTCG 240
 ATTCCTACTG CCCCTGCCAT GGCGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300
 10 CCGACATTCG AGGGTTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360
 GGTAAGGCAA CGGACTTTGA CTCCGTCACT CGTTGGTTTCG 400

(2) INFORMATION FOR SEQ ID NO: 3724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60
 25 ATATGGCGTG CGTCGTTTTG ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120
 AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TTnGTCATTC 180
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240
 TGGGTGCGGG TATTAAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

(2) INFORMATION FOR SEQ ID NO: 3725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420
 5 CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGCGC TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60
 20 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTITAGAC 180
 CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240
 25 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360
 30 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

(2) INFORMATION FOR SEQ ID NO: 3727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60
 ATGGGCGAAC AGCAAACCCCT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120
 45 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180
 GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240
 50 GTCTTTCGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCCTTATG CCTTTACACT 300
 CTATGAATGA TTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTITAGGAG 360
 GCGAACGGCC CCAGTTCAAA CTGCCCCCCT GAACACTGTC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG 60
GTGTGTCATT TGAGTGTCCA ATCGGTGCGA CGATTGCGAT TATCGGAGAA AGTGGTAGCG 120
GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTTGTGTAA 180
CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT 240
TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG 300
TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT 360
TGGAAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC 60
TTATATAGTT TGTAATAAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 120
TGCAAAAGC CGCTCTCCCA GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA 180
GACAGGTTCG AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC 240
TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA 300
AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC 360
CGGAATCGAA CCnGTAGTGA ATCACTCACC GCAGATTTTA 400

(2) INFORMATION FOR SEQ ID NO: 3730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

| | | |
|----|--------------------------------------------------------------------|-----|
| 5 | ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT | 60 |
| | CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CTATGTTTCC | 120 |
| | ACCATTTTTTA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC | 180 |
| 10 | GCGTTATTAA TCTTGTGAGT GTTCTTTCGA ACACTAGCGA TTATTTCTTA TGAATTCAAG | 240 |
| | CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTAATTACTT | 300 |
| | ATCTAGTTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT | 360 |
| 15 | GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3731:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| 20 | (A) LENGTH: 401 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG | 60 |
| 30 | TGGAGAATGA CGGGTTCGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCCAGCT | 120 |
| | GAGCTAATTC TCCGATTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC | 180 |
| | GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT | 240 |
| 35 | CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT | 300 |
| | AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAA GTCTTCGATC GATTAGTATT | 360 |
| 40 | CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T | 401 |

(2) INFORMATION FOR SEQ ID NO: 3732:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| 45 | (A) LENGTH: 397 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

| | | |
|--|-------------------------------------------------------------------|-----|
| | CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA | 60 |
| | TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT | 120 |

55

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240
 ATATTTATTA ACTGGTGACT TAGCGAGATG GACAACGATG GCGATATATT TATTATTGAC 300
 5 CGCAAAaAAG AaTTAATCAT AACTGGTGGc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

(2) INFORMATION FOR SEQ ID NO: 3733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120
 AAGACGGCAA AGTGGGTCTT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240
 ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300
 TACCAGGTAT TTTTGCAGCA GGNgATGTTT GCGACAAAGG TTACGCCAAA TTGTCACTGC 360
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60
 45 CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120
 TTGATAAACA GTCGCTTGGG CCTATTCATC GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180
 CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 240
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT 300
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGAcT CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCCT CAAAATTAT ATGGACCTTG CAGACTCGAA 60
 CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120
 TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA 180
 TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240
 TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCCAGCT 300
 GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGGAAGA CAGGATTCGA ACCTGCGACC 360
 CCTTGGTCCC CAAACCAAGT GGTTTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAATAA TGGCGGAGGA 60
 AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCT GTTTTCAAGA CCGATCCCTT 120
 CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAATT ATAAAATTAA 180
 ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240
 CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 300
 TTAAGCCCCT GTCGGTTTTT AAGACCGATT CCTTCAGCCG GACTTGGGTA nTCnTCCAAA 360
 ATTATATGGA CCTTGCAGGA CTCGAACTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

| | | |
|----|--------------------------------------------------------------------|-----|
| | TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC | 60 |
| 10 | AAGTGCTCTA CCAAGCTGAG CTAATTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC | 120 |
| | CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT | 180 |
| | TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA | 240 |
| 15 | TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG | 300 |
| | ACGGGATTTCG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTTT | 360 |
| | CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

| | | |
|----|-------------------------------------------------------------------------------|-----|
| | AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG | 60 |
| | CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGA _n CT | 120 |
| 35 | ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT | 180 |
| | GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA | 240 |
| | GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG | 300 |
| 40 | CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT | 360 |
| | TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

55

CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAA CCGACATCTT 120
 TAATTAATTG CTnTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180
 5 TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAAA TAACTGATTC 240
 GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300
 CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360
 10 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCGCAAG CCATTTTCTT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCaTT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240
 30 TACCATCGAC GCTAAGAACC TTTCTTGA CT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 360
 35 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTCTtTG TGTtTGCTTT TrA 413

(2) INFORMATION FOR SEQ ID NO: 3741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGTCTCTCT CGTACTAAGG ACAGCTCCTC 120
 50 TCAAATTTCC TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180
 GCTCGCGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360

ACCGGATCAn TAAGTCCGTC TnTCGACCCT GnTGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60

TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120

CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180

CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTTCTCCAC CATTTATTCT 240

TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300

GGTTCAAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360

GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60

TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120

TGTATGTAGT ATTGTTACGT TCTTGTCCGA AATAACGATA CACTTGCGTT TCTTTACCAA 180

CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240

TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300

CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360

ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10 CTACTGATTA CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60
 ATGGTGGAGA ATGACGGGTT CGAACCGCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120
 AGCTGAGCTA ATTCTCCGAT TTAAACTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 180
 15 GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240
 ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT 300
 AAGTAAAAGT GATTTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360
 20 TCAGCTCCAC ATGTCACCAT GCTTCCAnCT CGnACCTATT 400

(2) INFORMATION FOR SEQ ID NO: 3745:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60
 35 AAAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACACTA GCGATTATTT 120
 CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA 180
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240
 40 CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300
 TTAATGCATT GTCTAACAAC CGCTTGCTTT AAAAAGAATA GATTGnCAAG CGCTCGCATA 360
 AGCAATATCA CTTnAACCAA AAAATA 386

45

(2) INFORMATION FOR SEQ ID NO: 3746:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 677 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTCGTACCG AnaACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240
 TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300
 10 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420
 15 tTACCAATTc AGACAAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480
 TGATAAGGTC CGTGTTTCGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600
 20 CCATCATTTT AAAGAGTGCG TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCACG GTATTGCCTT TGAATCGCAT GCACAAAATA 60
 TGATGCTCAT TCATGAAAAT GGTGCGCCTA CACGTATTGC CTTAAAGAT TTCCATGATG 120
 GTGTTCGTTT TAAGCGTGAc ATTAAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180
 40 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240
 AGTACGCGAC TTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300
 45 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360
 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATAACTA TCCAACCATT CGGTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

5 ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60
 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGTCTTCG 240
 10 ATCGATTAGT ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360
 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400
 15

(2) INFORMATION FOR SEQ ID NO: 3749:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AACTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTtTACTTT TTATTTTGAC 120
 30 GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180
 TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTAATCATT 300
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360
 35 CCCAAGCCAT TTTTCTTTG TGTtTACTTT TTAATTTTGA 400

(2) INFORMATION FOR SEQ ID NO: 3750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

50 ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC 60
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240
 ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTtagAC ATAAAAAAAA GAGACCTTGC 300
 5 GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

20 CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGC ACTATAA 60
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120
 CCGCTGAACT ACTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTnA 180
 25 GnATTCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
 GGATTCGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300
 30 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAACCCCC AACCTACTGA TTACAAGTCA 360
 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

45 TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60
 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120
 CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180
 50 GGCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240
 AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATa 300
 AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360

(2) INFORMATION FOR SEQ ID NO: 3753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 120
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 180
 TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 240
 TTACTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC 300
 TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA 360
 TCGACGCTAA GAACCTTTCT TGA CTGGTGA CAAnCGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 3754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGA CTCGnACCAC 60
 CGACCTCAGC CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCC ATTAAATTGA 120
 ATGAnCAAAC ATTCAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG 180
 ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC 240
 TTGTTACGAC TTCACCCCAA TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA 300
 CTCCACCGGC TTCGGGTGTT ACAAACTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC 360
 GGGAACGTAT TCACCGTAGC A 381

(2) INFORMATION FOR SEQ ID NO: 3755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60
 CCCC GTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120
 CATGAAGTTA CGTTCTTTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTCT 180
 10 TTCGAACATA GCGGATTATT TCTTATGAAT TCAAGCTTAT TTAAAACTCT TTATTCACCTC 240
 GGTTTTGCTT GGTAAAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360
 15 AATATTTGGA ATGTTnAAAT AAACATnCAA AACTGAATAC 400

(2) INFORMATION FOR SEQ ID NO: 3756:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180
 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240
 35 ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTTCCGGn GGGGnACACG 300
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG ATTTGTCTGA 360
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

(2) INFORMATION FOR SEQ ID NO: 3757:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

55 GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC 60

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180
 TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAAGT 240
 5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300
 AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAArTtGG GAAtCTCATC TTGAGGGGGG 360
 gCTCATGCTt AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420
 10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

(2) INFORMATION FOR SEQ ID NO: 3758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60
 25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTAAAAAGA ATAGATTGTC 120
 AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA AATAAACATT 180
 CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240
 30 ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300
 ACCCCAATCA TTTGTCCAC CTTGACGGC TAGCTCCTAA AAGGTACTC CACCGGCTTC 360
 35 GGGTGTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

(2) INFORMATION FOR SEQ ID NO: 3759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CTTGCAGGA CTCGAACCTG CGACCGAACG 60
 50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACTA 120
 ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180
 TAGCCAGCTG AGCTACACCG CTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360
 AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

5 (2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60
 ACCAGAGGTA TGTCCATCCC GGTCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120
 20 CGCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTT TGAACCCAGC TCGCGTACCG 180
 CTTTAATGGG CGAACAGCAA nCCCTTGGGA CCGACTACAG CCCCAGGATG CGATGAGCCG 240
 ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTTTG GGGGAGATAA GCCTGTTATC 300
 25 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GnCCTTnCAT GCGGAACACC GGATCACTAA 360
 GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 623 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

40 TATGTATTTT ATAATGTACA GCTCGTTGAn TCnTATTTTT CCTTATATTA AGTGCCATTA 60
 ATACAAAACC TAGCTCTCGT TTAACCTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120
 CAAAATAGCC TTCATAAATC CAAAACAGG CTCTACATCA ATTTTTCTTT GACTATAGAT 180
 45 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240
 ATAATCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300
 AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360
 50 ATCATTACGG TATGCATATC TTTTAAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420
 ATCATTAAGT TCGTCATATT TCCAATTTTA AGTGTTGAAA ATGTCACTTT TAACTTTCT 480

55

AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600

AATAACCGAG GGATTGTTGG AAT 623

5 (2) INFORMATION FOR SEQ ID NO: 3762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAA TAGTTCTTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60

AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCGA ACCTCTGACC 120

20 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180

CTGGATTCGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240

CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300

25 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360

CaAAATGGTG GaGAATGACG GGTTCTGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420

TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480

30 CCGTGAAAGG GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540

CGAACCTTAC GACCGATCGG TTTAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600

35 ATTAATATTA TGCCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660

ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

50 TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60

AAAAATGGAG CAGAAGACGG GATTCGAACC CGCGACCCCA ACCTTGGCAA GGTGTATTTC 120

TACCGCTGAA CTACTTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

55

AGGATTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300
 GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360
 5 CAATTGCTCT A_nCAATTTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCGA ATTTGGTTTC 60
 20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120
 CGTTTAA_AAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180
 TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240
 25 CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300
 TTATTAA_AAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360
 ACAATATACT CTGGTAAATA ACCGA_AGGaT TTTGAATCAT TGTTAA_AAAT GGGATTAATG 420
 30 TTCTAGTATC TGTTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTG_r GAATTTGTCTG 480
 CTATTTG_gTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540
 35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCC_nG TTTTAGGAAA ACCTAATTCC 600
 AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTTGGTG CTGCATATCC CCTACAATAA TTAAACCTTT TTTCTTATTT AAAATGTGTC 60
 50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120
 ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAA_AAATGAA 180

CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGCGCCT ACAnTTCTTA ATTCAGCGGA 360
 5 CGGTCACTTG TTAAAACGGT TTAAGGTATT CTACTAATTn 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTrGTA 60
 20 tCTCACGCAA tCTTGGTGGT CATTCAAGTC GTATATGGCA TCCATTAAGA CGCGAAGATC 120
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAATACA GTGTCTCGCT CTGTTTCTGC 240
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTCGCC 300
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360
 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420
 30 TTCTTGGCAT ATTCATTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60
 45 TGTCCAATTG AAACACCTGA GGGACCAAAC ATTGGATTGA TTAAGTCATT ATCAAGTTAT 120
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180
 50 CATGCTATCA CTGATCAAAT TGAATATTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240
 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTCGTTTCA TGGATGATGA AGTTGTATGT 300
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAAA TGGATTATAT GGATGTATCG 360

(2) INFORMATION FOR SEQ ID NO: 3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTTAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT 60
 ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG 120
 CTTAACTTCT GTGTTCCGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT 180
 ATGAATGTAA TTTATACATT CAAAACTAGA TAGTAAGTAA AAGTGATTTT GCTTCGCAAA 240
 ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG 300
 CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG 360
 AAATCTCATC CTGnAGGGGG CTTTCATGCTT AGATGCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT 60
 CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA 120
 ATCTTTCTnC TGCACTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA 180
 CGTTACCAGC AATAATTTCA TTTTGTCGTT CTTCAAAAGG TGCTTTGACA ATGACCGTAC 240
 CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAGC 300
 CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTTCGTATA AACATTAATT 360
 GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA 400

(2) INFORMATION FOR SEQ ID NO: 3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TTAAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300
 AGTGGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

(2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60
 30 GGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180
 GCTTGTTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300
 TCGTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTTG 400

(2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC GGTCTCAATG CGGCTCATCG 60

55

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240
 5 GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTGTGCTTT TTATTTTGAC GTTTTAGACA 300
 TAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCCTGGGCA 360
 ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTTCACAC 180
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

(2) INFORMATION FOR SEQ ID NO: 3774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 120
 CTTTCCTCTC CTTTCGGCTCT CACTTACTCA TTTAGCTCTA CTAAACTCGT TCGGTTCTTT 180
 50 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240
 TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAAA TGCGGCTCAT 300

GACGCTAAGG AGCTTAAACT TCTGTGTTTC GGCATGGGGA

400

(2) INFORMATION FOR SEQ ID NO: 3775:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

| | |
|--------------------------------------------------------------------|-----|
| CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC | 60 |
| TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT | 120 |
| TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA | 180 |
| TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAAACA CGTGAACGGC TCAAATGGAA | 240 |
| GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC | 300 |
| CAACATTGG ATTGATTAAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA | 360 |
| TTGAAACACC ATATCGTAAA AGTTGATTTG GntACACAGC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3776:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

| | |
|-------------------------------------------------------------------|-----|
| AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG | 60 |
| TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA | 120 |
| GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA | 180 |
| CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT | 240 |
| AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACnTAG GCGATTATTT CTTATGGAAT | 300 |
| TCAAGCTTAT TTAAAACTCT TTATTCACCT GGTTTTGCCT GGGTAAAATC TAnATTTTAC | 360 |
| TTACnTATCT AGGTTTTCAA TGTACAAATA ATGGTGGGGC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3777:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TCGGTGACAG | 60 |
| 10 | GCAGGCGTGT TAACCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA | 120 |
| | ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG | 180 |
| | GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG | 240 |
| 15 | AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT | 300 |
| | AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA | 360 |
| | GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

30

| | | |
|----|-------------------------------------------------------------------|-----|
| | CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGC AGTCATAGTG CCGTCAGCTT | 60 |
| | TAAATACTGT ACGTAATTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT | 120 |
| 35 | CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA | 180 |
| | CTTGTATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT | 240 |
| | GaTGACTTCT GACAGCATAA GCATCTTGaT CTTCGCGTGA TACGTCAAAT TGGGATGCTA | 300 |
| 40 | CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCaA TTGTAAGGTT | 360 |
| | GGATTGTTTG TGGGCTTCGT TnGCCACCnn TTGGTACGGC | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

55

CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120
 CTCGGTTGAA ACCTTACTTA TTCATTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTCGAT GTATCATTTG GGTTTAGCAA 300
 ACAGCCATAA CCTTCGTCAT ATAAATGTTC ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

(2) INFORMATION FOR SEQ ID NO: 3780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGCACACn CAGGCGTGTT 60
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTTCGAA CCCCCGCGAG 120
 CCGTTAAGCC CCGTTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180
 AAAATTATAT GGACCTTGCA GGAATCGAAC CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360
 35 CCGCCTTATA TAGTTTGTAATAAATATGGT GGAGACTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAAC ATTAATAAAC CGCCTGATTC 60
 TCTAGCACGT TCATAAATAG TTAATTGATA TCCTAGTAGA TTAAGTTCTT CAGCAGCAGC 120
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTTTCA TCTCTACGGC GACTCGGAAC 180
 TTTCGGCGCT ACCCAACCAT TTTCAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTTCGCTT AAGCGTCATA AGCAGTTTTA 360

AAATCTTGAT GATACACCAA GTCGTCCAnT CAGGATGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60

CATTGATAAA TCGCTTGAAA TGTGCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120

TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180

ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240

CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300

AGGGGTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAGATGC CATTGCCTAA 360

ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

AATCGGGTGA TGTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60

TGGATAACTG TTTTAAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120

TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180

CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAAT TAAATCGCTG TTGTCCACAT 240

AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300

CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGAnTT 360

ACAAAATCTT CnAAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTACTAAGA TGTTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCGGA AATCTCTGGA TCAAAGCTTA 120
 CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300
 TTTAAAATAA TTAACTCAT TGTCTGCnAA ACGTTTTCTT TTATAAAAAG AnTTTAAACG 360
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnnGA 400

(2) INFORMATION FOR SEQ ID NO: 3785:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60
 35 CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180
 TTTCGCAATT TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300
 CTGAAATAGT TGACTIONGCA TTTTGCGCTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

45

(2) INFORMATION FOR SEQ ID NO: 3786:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTACTAG 180
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTTAC GACGTGTTAC 240
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCGCC ATAATACCTT TTTCAACCAC 300
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

TCTCTTCCCG TTTGCTCGC CGCTACTAAG GGAATCGAAn TTTCTTTCTC TTCCTCCGGG 60
 TACTAAGATG TTTGAGTTCT CCGGGTGTGC CTTCTGATAT GCTATGTATT CACATATCGA 120
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTGCGAAA TCTCTGGATC AAAGCTTACT 180
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 300
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTTAACG CGTTATTAAT CTTGTGAGTG 360
 35 TTCTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGACTA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120
 TTTTGATGA TTCTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTTT 180

TCTTCTGCAA ACAACAAACT ATTTTATTATA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300
 CTAGCTGCTA AaACATTATA ATCAGCTGGA TGTTGATGCT TTAACCTCCTC TGTTTTAGCT 360
 5 AATGGAGATT TTAAACGATC TACATTTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60
 20 AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120
 CGGTGTTTTT GGCGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTG TCCCTATTGT 240
 25 CACAGCATTG GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTGGC CAAGCATACA 300
 nGCCGGCATT TATCATGTTG GTGGGATTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360
 TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

30 (2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60
 TTAAATTAT ATACCCACCA CATTTGGTGA kGAACCTAAA AAAAAGCACT TCCCAAAAAT 120
 45 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300
 50 AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

55

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTGnTCTT 540
 AACCGtTGAC CAAGGAGCCA TGGCTCaCcA GGTA_gGACTC GAACCTACGA CCGATCGGTT 600
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660
 CTACTCTAGC GGAACTAAAG TTnGAACTnA CCATCGACGC TAAAGGAGCT TAACTT 716

(2) INFORMATION FOR SEQ ID NO: 3791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

20 TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTTA AAGGTAACAC TATCATTTAT 60
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120
 ACGTGTACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180
 25 AACAGCACAT CAGCTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240
 AATTAATGAG GATTTGGAAA CATTCTTTGC nTGATTTTCA AACATTAGCT GTGATCGGTA 300
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360
 30 CTTATGTCGT TGTTAAAACA AATTTTGAAA AAAGGAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTCACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180
 TGTA_gCTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAATT TTGTCATGAT GTGCCTCCTT 300
 ACCGTATGAT GTtATTCAAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA

425

(2) INFORMATION FOR SEQ ID NO: 3793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG | 60 |
| | AGTGACGGAG NAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG | 120 |
| | GAGGGGGGCA GATTGGAAC TCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA | 180 |
| 20 | GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG | 240 |
| | ACGGGTTTGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT | 300 |
| 25 | CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTTA CCGCCGTGAA AGGGCGGTGT | 360 |
| | CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

| | | |
|----|-------------------------------------------------------------------|-----|
| 40 | ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC | 60 |
| | TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA | 120 |
| | TGTnTCACAA CGTTACCATT ACGTTTAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA | 180 |
| 45 | CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT | 240 |
| | GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA | 300 |
| | GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC | 360 |
| 50 | CACATTCGGT TTATTCATAG CGGACCAGTT TGCCTCCATT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA | 60 |
| 10 | TGGTAGGAGA GCGTTCTAAG GCGGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG | 120 |
| | AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT | 180 |
| | AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC | 240 |
| 15 | AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT | 300 |
| | GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTGATTG CACGTCTAAA GCAGTAAAGC | 360 |
| 20 | TGAGTATTAG GCnAATCCGG TACTCGTTnA AGGCTGAACT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA | 60 |
| | ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG | 120 |
| 35 | CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA | 180 |
| | AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTCATCTAC | 240 |
| 40 | TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC | 300 |
| | AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC | 360 |
| | AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAGTG ACGCTGATGT GCGAAACGTG 120
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180
 5 TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240
 CGACCGCAAG TTGAAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300
 GTTTAATTCG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACACTCTAG 360
 10 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 3798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60
 25 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180
 AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TCGACATAT GGGCCTAGAG 240
 30 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAAA CATTACGTAT 300
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 3799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTCGCCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60
 50 CGTTACTTGG TTTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTGCCT 180
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

TTTtagTGCG TTACTGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTn TTTTCGGTGC 360
 CATTAAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

(2) INFORMATION FOR SEQ ID NO: 3800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAAT GTGTTAGGTA AAGGTGTCAT 60
 TGTCGTCAAT GATGTGCCTG GCTTTGTGCG AAATAGAGTC GGCACGCAAA CAATGAATGA 120
 TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180
 GCAAGCGATT GGTCGTCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240
 TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAAGTACC TGAAGAAACA CCTTATTTTC 300
 ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAAnnCGnAA 360
 ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GGnAACTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60
 TAAATTGTAA AACGATAGTT CCCGTTGTTC CTAATAGTTG TATTCTATCT GACGCATAAT 120
 GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180
 TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACTTTAA TGTTTCAACT AGTTTTTCTG 240
 TCGTTAACAT GGGTTCACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300
 TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360
 TTATnATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTCACTTTT GAACCATGCG GTTCAAATG ATTATCCGGT ATTAGCTCCG GTTCCCCGAA 60
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCATGT ATTAGGCACG CCGCCAGCGT 180
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GTCATAAAT 240
 ACTAAATAAT GTTTGTAAC TATAGTTACG TTTTGTGAA TTAACGTTGA CATATTGTCA 300
 TTCAGTTTTT AATGTTCAAT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAAAT 360
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3803:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 60
 35 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180
 AACCGAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240
 40 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300
 TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360
 45 ACGGATAGGG ACCGAACTGT TTTCACGACG GTnCTGAACC 400

(2) INFORMATION FOR SEQ ID NO: 3804:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGCGTCTGCC AGTTCCGCCA CCCCGGCACT 60
 ATAAAAATGG AGCAGAAGAC GGGATTTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180
 TTAGwATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240
 GAGGATTTCGA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCCAAC CTACTGATTA CAAGTCAGTT 360
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420
 15 TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

(2) INFORMATION FOR SEQ ID NO: 3805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTATT TTGACGTTTT AGACATAAAA AAAGCTCAGG GTCTCAACTT GCCTGGCAAC 60
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240
 TTCTTTGTGT TTACTIONTTTA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 35 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGGCAACGT TCTACTCTTA GCGGAACGTA 360
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGACTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60
 TTTACTGAGT CATTGCACTT ATCATAACA TTATATTAG CATGAGTTAT ATTACTAAAA 120

TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTA CTGCCAA 240
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTTGCTCG AAGTTCAGAT CGCTTTTACA 300
 5 ATTGGGcnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGA ACTA TTCGTCTATT AAAAGCGATG 120
 TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTTCGTG CAAGTTATGG 300
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

(2) INFORMATION FOR SEQ ID NO: 3808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

ATGCGCAGAG TATATGGAGG AACACCAGTG TCGAAGCGCA CTTTCTGGTC TGTA ACTGAC 60
 45 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAACTCA AAGGrATTGA CGGGGACCCG 240
 50 CAcAAGCGTG GGAGCATGTG GtTTAATTCTG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTGCCA TCATTAA

447

(2) INFORMATION FOR SEQ ID NO: 3809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

| | | | | | | | | | | | | | |
|----|-----|-----------|-----|-----------|-------|-----------|-----|-----------|-----|-----------|-----|-----------|-----|
| 15 | CCA | ACTGAGC | TAC | TGAACCA | TAATA | AAAAT | GTA | ATGACTG | GCG | GTCTCGA | CGG | GAATCGA | 60 |
| | AC | CGCGATC | TC | CTGCGTGA | CAG | GCAGGCG | TG | TAAACCGC | TAC | ACTACGA | GAC | CTATAAA | 120 |
| | AT | ATTGCGGG | AG | GCGGATTT | GA | ACCACCGA | CCT | TCGGGTT | AT | GAGCCCGA | CG | AGCTACCG | 180 |
| 20 | A | ACTGCTCCA | T | CCCGCGATA | A | TAAAAAATA | A | TGGCGGAGG | A | GAGGGATT | C | GAACCCCGG | 240 |
| | C | GGCCCGTTA | A | GGCCCTGTC | G | GTTTTCAAG | A | CCGATCCCT | T | CAGCCGGAC | T | TGGGTATTC | 300 |
| | C | TCCATTATT | A | TAGGTAAAT | C | GCTATTAAT | T | AATAAATTA | A | ATGGCGGTC | T | CGACGGGAA | 360 |
| 25 | T | CGAACCCGC | G | ATCTCCTGC | G | TGACAGGCA | G | GCGTGTTAA | | | | | 400 |

(2) INFORMATION FOR SEQ ID NO: 3810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

| | | | | | | | | | | | | | |
|----|---|-----------|---|------------|---|------------|---|------------|---|-----------|---|-----------|-----|
| | T | GCTTGGTAA | A | ATCTATATT | T | TACTTACTT | A | TCTAGTTTT | C | AATGTACAA | A | TATGGTGG | 60 |
| 40 | G | CCTAAGTGG | A | CTCGAACCA | C | CGACCTCAC | G | CTTATCAGG | C | GTGCGCTCT | A | ACCAGCTGA | 120 |
| | G | CTATAGGCC | C | ATTTTTTTTG | A | ATGTTAAAT | A | AACATTCAA | A | ACTGAATAC | A | TATGTCAC | 180 |
| | G | TATTCCGC | A | TCTTCTGAA | G | AAGATGTTC | C | GAAATATATC | C | TTAGAAAGG | A | GGTGATCCA | 240 |
| 45 | G | CCGCACCTT | C | GATACGGC | T | ACCTTGTTA | C | GACTTCACC | C | CAATCATTT | G | TCCACCTT | 300 |
| | C | GACGGCTAG | C | TCCTAAAAG | G | TTACTCCAC | C | GGCTTCGGG | T | GTTACAAAC | T | CTCGTGGTG | 360 |
| 50 | T | GACGGGCGG | T | GTGTACAAG | A | ACCCGGGAAC | G | nATTTCACCG | | | | | 400 |

(2) INFORMATION FOR SEQ ID NO: 3811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GCTTCATGCT TAGATGCTTT CAGCACTTAT CCCGTCCACA CATAGCTACC CAGCTATGCC | 60 |
| 10 | GTTGGCACGA CAACTGGTAC ACCAGAGGTA TGTCCATCCC GGTCCTCTCG TACTAAGGAC | 120 |
| | AGCTCCTCTC AAATTTCTTA CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC | 180 |
| | TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTGGG ACCGACTACA | 240 |
| 15 | GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGGAACTCT | 300 |
| | TGGGGGAGAT AAGCCTGTTA TnCCCCGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC | 360 |
| | ATGCGGGAAC CACCGGGATT | 380 |

20

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

30

| | | |
|----|-------------------------------------------------------------------|-----|
| | GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG | 60 |
| | CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAACTG | 120 |
| 35 | GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT | 180 |
| | CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCACGAC GTTCTGAACC CAGCTCGCGT | 240 |
| | ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA | 300 |
| 40 | GCCGACATCG AGGTGCCAAA CCTCCCCGTC GntGTGAACT CTTGGGGGAG ATAAGCTGTT | 360 |
| | ATCCCCGGGT GAGnTTTTnTC CGTTGA | 386 |

45

(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

55

CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTTGGTAC TTCTGGTGTC 120
 GGTGGCGTTG GTGGCACCAGT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180
 5 TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240
 AATTGATAAC TTGGTTTATC TTTATTTGTA TCTTCTTCAA TAATTTTCACT GTGCTTATTG 300
 AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360
 10 TACTTAGGTT TGTCTTTTTT TGTAnCTTCC TCGAATGACT 400

(2) INFORMATION FOR SEQ ID NO: 3814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
 25 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCnACTA AACTCGTTGC GCnCTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180
 TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GCTCATCGCA 240
 30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300
 CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360
 TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

ITCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60
 3AATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120
 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180
 CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTAA AGCGATATAT TGATGTCTAG 240

GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360
 TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60
 GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120
 TTTACATTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TCTTTCTTTG 180
 TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360
 GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300
 TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360
 GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180
 15 CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240
 TTCTGAATAG GGCCTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300
 CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCCAATCGAA 400

(2) INFORMATION FOR SEQ ID NO: 3819:

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAA TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TCGGAGACCT 360
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3820:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TGGCTCGAAC CACCGACCTC ACGCTTATCA GCGTCGCTC TAACCAGCTG AGCTATAGGC 60
 CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180
 ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGTC CCACCTTCGA CGGCTAGCTC 240
 CTAAAAGGTT ACTCCACCGG CTTCGGGTGT TACAAACTCT CGTGGTGTGA CGGGCGGTGT 300
 10 GTACAAGACC CGGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

(2) INFORMATION FOR SEQ ID NO: 3821:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

TATTAAATTA ATGGTGGGCC TAAntGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAAACTGA 120
 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180
 30 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTTAC 300
 35 AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360
 GCTGATCTAC GATTACTnAG CGnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60
 50 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120
 GCAGATTCGA ACTGCCGAAC CCGAAGAGCG GATTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180
 GCTCTGCTTT TTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300
 TCTCATGTTC TCGAGATCCA CCAAATGTnA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180
 ACGCGTTATT AATCTTGTGG AGTGTCTTTT CGAACACTGA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAACTCTT TATTCAC TCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 50 ACnTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60
T TACTTACAG CTCCCCAAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120
CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180
GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240
TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATnTT ACTTACTTAT 300
CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360
CCAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTnTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60
AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120
ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180
TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300
TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360
CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

5 AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTAG AGAAGACCAA AAGAAGAAAA 60
 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AAACAGAGAA AATATAAAGA 120
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AACTTAAAC TGGTGAAGCC TTTAGTAAAA 180
 TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240
 10 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGGG AAAGCTTGGC CAATCTGTTA 360
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3828:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

25 TCTCAGTTCC AGTGTGGCCG ATCACCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60
 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180
 AAGTTATCCC AGTCTTATAG GTAGGTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240
 35 TCAGAGAAGC AAGCTTCTCG TCCGTTGCT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300
 GTTCATCCTG AGCCAGGATC AACTCTCCA TAAAATTAT GATGTTGANT AGCTCATAAA 360
 TACTAAATAA TGTTGTAAC TATAGTACGT TTTTnGAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3829:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

50 CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60
 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAT 120

55

ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTCGATT 300
 5 CAAGTGGGAR sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTC 400

(2) INFORMATION FOR SEQ ID NO: 3830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCCG AAATCTCTGG ATCAAAGCTT 120
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 25 GGATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTFA TAAGTCAAAC 240
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT 300
 TTAAAATAAT TTAATCATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 60
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120
 CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT 180
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300
 TTTTTTGCCT GGGCAACGTT CTACTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

(2) INFORMATION FOR SEQ ID NO: 3832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCAC TC TGGTTTTGCT TGGTAAAATC TATATTTTAC 60
 TTACTTATCT AGTTTTCAAT GTACAATTTC TTTT TAGTCA AGCGCTCGCA TAAGCAATAT 120
 CACTTTAACC AAAAAATATT TGAATGTTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180
 ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 300
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360
 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT 60
 TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT 120
 TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCAAT GATACCAGTT 180
 AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTATA ATGTGTTAAA 240
 TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATAT ACGGGTTACC 300
 AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTAAA 360
 AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5 NAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CCGTTATGAG CCGTTAGCTC 60
 TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180
 10 CGCCTTATAT AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240
 TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300
 GGAAGACAG GATTCTGAACC TGCGACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG 360
 15 AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA 400

(2) INFORMATION FOR SEQ ID NO: 3835:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60
 30 CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120
 AGGCGGAGGA ATCACATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180
 AAAAAATTAT GGTCGATTGC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT 240
 35 AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300
 GCAGATGCCT TGTCAGGTGA AGACATCACG TATCnAGAAG CGTGGGCAGA TGAAGAATAT 360
 40 CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

(2) INFORMATION FOR SEQ ID NO: 3836:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

CTAATCGCAT CTTTTTCAAT CTAAGTGCGT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60

55

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360
 10 CAATTGTGGC AGCTTTTTnC TTCCGGnGAA AATATCnGGC 400

(2) INFORMATION FOR SEQ ID NO: 3837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGA CCAAGGAGCC ATGGCTCAAC 240
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGGAAGTAAn TCGGACTACC 360
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 60
 GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT 120
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240
 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

TCAGATCCAA ACGTTTTCA_n TCG_nCCAAGC CAATTTGCCT

400

(2) INFORMATION FOR SEQ ID NO: 3839:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

| | | |
|----|-----------------------------------------------------------------------------------------|-----|
| 15 | TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGA _c rC GACTCCTCTT | 60 |
| | AACCTTCCAG CACCGGGCAG GCGTCACCCT gATA _c ATCAC CTTACGGTTT AGCAGAGACC | 120 |
| | TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC | 180 |
| 20 | TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCA _t TTTG CCGAGTTCCT TAACGAGAGT | 240 |
| | TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGG _c ACC | 300 |
| | TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACT _c GAg GACACAATGT | 360 |
| 25 | CTTCTCCCCA TCACAG _t TCA GCCTTgAACG rGTaCCGGAT TTG _n CTAATG ATTCAG | 416 |

(2) INFORMATION FOR SEQ ID NO: 3840:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

| | | |
|----|----------------------------------------------------------------------------------------------|-----|
| 40 | AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT | 60 |
| | TCCTCTCCTT CGGCTCTCGC TTA _c TCA _t TTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT | 120 |
| | CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTCTTTTGT GTTTACTTTT | 180 |
| 45 | TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAA _a ACTTG CCTGGCAACG | 240 |
| | TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT | 300 |
| | GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCA _t TTAG CTCTACTAAA | 360 |
| 50 | CTCGTTGG _n G CTCTTTTCTT CGGTTT _n GTC AGAnTTCAAA | 400 |

(2) INFORMATION FOR SEQ ID NO: 3841:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA 60
10 ATTCCTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA 120
TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG 180
ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG 240
15 CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT 300
AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTTG TAGTGGTGAA 360
GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA 400

20

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

TCGCGATTCTG CGTGTTTCAGA AATCATCGGC ATCGCGTCAT TCAATGATTC ATATGCATCT 60
AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA 120
35 TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT 180
CCTTGTCTGA CATTTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT 240
GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA 300
40 CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTT 360
AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC 400

45

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

5 GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCn GTCGAACACG GACCTTATCA CCCATGTTCT 180
 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240
 GGCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300
 10 CTATTTGCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360
 TCATCCGnTC ACTTTCAACG TAAnTCGGGT CGGGTCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 3844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

25 ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60
 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360
 35 AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTTAT TTTCTGCATT 420
 TTTAATAGTA TCGTGTTTAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

(2) INFORMATION FOR SEQ ID NO: 3845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

50 GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60
 GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TGCGTAGAGC AATTGCGnAA 120
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

TTAACATTCT TACCTTATGT TGTTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60
 20 TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 120
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTAT 180
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300
 AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 360
 30 GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAGG TATTACGATG 60
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120
 45 GCACGTCCAT TAAGACGTAT TGTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240
 50 AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAA AATGAGCATC AGGTCGCCCT 300
 TGCCTGTGGC TCATTTTTTT GAATTATTC CCTGGGAAA TGATTCGCTG TGTGCTGTTT 360
 TGTTCACACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

TTTAAAACTC TTTATTCACT CGGTTTTGCT TGGTAAAATC TATATTTTAC TTAATTATCT 60
 AGTTTTCAAT GTACAAATAA TGCTGGGCCT AAGTGGACTC GAACCACCGA CCTCACGCTT 120
 ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCATC TTTTGAATG TTAAATAAAC 180
 ATTCAAAACG GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA 240
 TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTTGGTnACG 300
 ACTTCACCCC AAATCATTTG TCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC 360
 GGCTTCGGGn GTTACAAACT CTCGTGGGTG TGACnGGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 60
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 120
 TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 180
 TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 240
 AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG 300
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 360
 GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180
 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGGAAATTAT TAGGTGTACA AATGACCACC 240
 10 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360
 15 TCTTTGAGTT TCAGCAATGC TGGAAATATGA CGGTCTTG TG CAATACCACC AACAACTATG 420
 CACACCAACT TTTAAnTTTG TnCATGATGT GCCnGCTTnA CCG 463

(2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 628 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGATTCG ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120
 AACCCGAAGG AGCGGATTTA CAGTCCGCcG CGTTTAGCCA CTTGCTACC CCTCCAGCTT 180
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG CTCTACCACT 420
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn 600
 TTAGTAAGTA AAAGTGGATT TTGGnTTh 628

(2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCGAATT GGCCGTGTAG TAGCCGATAT 60
 ATTTGCCAAT GGTtATCAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTtAAA 240
 CATTtTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360
 15 ATTTGGAACG GCAAACtTTT TCCCAAGTGG TCCAAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3853:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

25 TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60
 30 TCATAAGAAA TACTAATTTC TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120
 TGCACATTAT TGTAAGCTGA CTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTTGCACATT 240
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CA CCCCAACTnC GCATTGCCTG 360
 TAGAATTtCT TTTCGAAATT CTCTGTGTTG GGGGCCCA 400

(2) INFORMATION FOR SEQ ID NO: 3854:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAAACGA AGCAATTAAT 60

55

GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300
 TTAAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360
 CAGTTGCAAA TGnTATTGTC AGCCACGAGT ACGGCTGGTA 400

10 (2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60
 AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120
 25 TTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180
 GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATThAA TAAACAGCCT 360
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

45 CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60
 CTATTTCTTC TATTGTAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTTCGAT TCGTGATTTT 180
 50 GAATACTTTT CTTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAGTGA 300

TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTGA | 60 |
| | AGTTGTGAAT GCACATGGTA AACATTTTGT TGCATTACCA CGTGAAGATG AAGATATTGC | 120 |
| | AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA | 180 |
| 20 | TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT | 240 |
| | AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC | 300 |
| | TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCTT GCCGAGTAAT | 360 |
| 25 | TGTCAAATGT ACTATGCAAT G | 381 |

(2) INFORMATION FOR SEQ ID NO: 3858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG | 60 |
| 40 | ATGAGGTAA TAGGTTTCGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT | 120 |
| | CGATCGAAGA CTTAATCAAA ATAAATGTTT TCGGACAATT CACTTTTACT TACTATCTAG | 180 |
| | TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT | 240 |
| 45 | TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC | 300 |
| | GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA | 360 |
| 50 | GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA | 400 |

(2) INFORMATION FOR SEQ ID NO: 3859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

| | | |
|----|--------------------------------------------------------------------|-----|
| | GTTTATTAAT CGTGTCATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA | 60 |
| 10 | ATGTTAAATC TGTTTTAACA TTATTTTGAA TTTCATTTCAT GCATCTGAAT CTGAATCGCT | 120 |
| | ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA | 180 |
| | ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA | 240 |
| 15 | ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT | 300 |
| | ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA | 360 |
| 20 | ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA | 420 |
| | ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC | 480 |
| | CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG | 540 |
| 25 | CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG | 573 |

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| 30 | (A) LENGTH: 400 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG | 60 |
| 40 | CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA | 120 |
| | CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT | 180 |
| | ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT | 240 |
| 45 | CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA | 300 |
| | AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT | 360 |
| | TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGnGC | 400 |

50

(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| 55 | (A) LENGTH: 400 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3862:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

25 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360
 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

(2) INFORMATION FOR SEQ ID NO: 3863:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

50 TCGGCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 240
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 300
 TGTTTGCTTT TTATTTTGAC GTTTTAGACA TAAAAAAAG AGACCTTGCG GTCTCAAATG 360
 10 CGGCTCATCG CATnCATnT TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGT TATGGGAAAT GAATTAATGT 120
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240
 30 GAAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300
 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360
 TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

400

(2) INFORMATION FOR SEQ ID NO: 3866:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

15

AAGTCAATAA CTTTTTTTAT CTTGTCCATT TTATTTTSTA ACCAAAATTT GATTAAAAAA

60

CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA

120

GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA

180

20

TATGAATGTA AITTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA

240

AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT

300

GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT

360

25

TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG

400

(2) INFORMATION FOR SEQ ID NO: 3867:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA

60

40

TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC

120

TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTCGTTGAT TTCACACTGC CGAGAAAAGC

180

CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT

240

45

CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG

300

AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT

360

50

GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA

400

(2) INFORMATION FOR SEQ ID NO: 3868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTTGA TCACTGTTTA | 60 |
| 10 | GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT | 120 |
| | GTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT | 180 |
| | GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAGGT | 240 |
| 15 | ATTAGTACTT ACTTTAAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA | 300 |
| | GGTGCCAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA | 360 |
| | AnTCGATAAA TTTGTGGACG GTG | 383 |

20

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA | 60 |
| | CGACAACCAC CACCTGTCAC TTTGTCCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA | 120 |
| 35 | GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG | 180 |
| | nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG | 240 |
| | GAGTGCTTAA TCGGTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC | 300 |
| 40 | ATCGTTTACG GCGTGGAATA CCAGGGTATC TAATCCTGTT TGATCCCCAC GGTTCGCAC | 360 |
| | ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTTCGAA 300
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360
 10 GCTTGGTAAA AGCnnGn 377

(2) INFORMATION FOR SEQ ID NO: 3871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCCTCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACCTGCA ACTGGTTTAA CTGTATTACT 240
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360
 35 GCGAGTTACn GGGGTCCAAA CCCnTGGTGT AAAAnCGAAC 400

(2) INFORMATION FOR SEQ ID NO: 3872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360
 CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60
 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120
 GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180
 CAAnnGTTTT CAATCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240
 GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300
 GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 480
 GCCATTTTTT TTTGTGTTTA CTTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540
 TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTTGCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTCTCTCTCC TTCGGCTCTC GCTTACTCAT 120
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240
 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

400

(2) INFORMATION FOR SEQ ID NO: 3875:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

15 TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120
 CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180
 20 CCGACATCTT TAATTAATTG CTTTGACAGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240
 GATGGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACCTTGC TGCATCAAAT 300
 AACTGATTCG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360
 25 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60
 40 TGGTGATCCT CAATTCGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCGTCA 120
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180
 CGCACGTACA GTGGTTGAAA AAGGTATTAT GGCGGCACTG CACGTnTTGC TCGGAAAAAA 240
 45 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360
 CCGGGGGGTC TACAAAATCT GGTCGTGACT CTAGACCGCA 400

50

(2) INFORMATION FOR SEQ ID NO: 3877:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC | 60 |
| 10 | CATCATGTTA TGTGATTGGA ATACTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT | 120 |
| | ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT | 180 |
| | TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT | 240 |
| 15 | ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACTTCTGG GnGTATCAAA ATGnTGCAAT | 300 |
| | GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC | 360 |
| 20 | TCAACACCTT AGGGGTAAAC TTCGGCCATA TCCCTTTTGG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

| | | |
|----|--------------------------------------------------------------------|-----|
| | ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TGTAGATGCA | 60 |
| | TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA | 120 |
| 35 | GAAGTTGCTG AAACTCCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA | 180 |
| | AACAACCTGGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC | 240 |
| 40 | TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG | 300 |
| | GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA | 360 |
| | CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

55

TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180
 5 GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240
 CTTGGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 300
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTGChTTT ATTTGACGTT 360
 10 TAGACATAAA AnAAGAnCCT TGCGGnCTCA ATGCGGCCAT 400

(2) INFORMATION FOR SEQ ID NO: 3880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180
 GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240
 30 ATGGATATTG ATTCGAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300
 CTCTCGGTCA TATTCAGGCA TATCCGGACA CAACTTGGAT AGCAGTTGTG ATTTCCCAGG 360
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

(2) INFORMATION FOR SEQ ID NO: 3881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180
 TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360
 ACAGGTAGTC CAAGATGGAG AntCTnAAGG TGGAGCGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60
 ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGCCCCTGA 120
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTT AGTCAACTAC TGCCAATATA 180
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240
 ATATTTAATT TGC GTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300
 TAAGTTTTC GAAATAAACC TATCTTAAAA TATAAAAAAA TCGAGAATTC GTAGTTTAAT 360
 AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACTAAA 480
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540
 AGATTCATAA TCTTCTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600
 CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA AACTTTTCAC CAATAGATAG 120
 TTATTTGTTG TTACGTGGAC TTAACACTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180
 CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGAg GTACKGAAAC ATTAGTGACC 360
 TTCCCTTACA CCCAAACACc GTTGATATGC CAGT 394

(2) INFORMATION FOR SEQ ID NO: 3884:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120
 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTCGATTAG CGTAACAAAA TATGGACCTG 180
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240
 ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300
 CAATAACGAC GCCAACACTA AAAAATCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360
 AAAGAGGAAT CACAAAAGTT CCnTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180
 TATAGGCCCA TTTTTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360
 GACGGCTAGC TCCCAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCATTGGA AACTGGAATn 120
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300
 GTTAGGGGGT TTCCGCCCCCT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360
 20 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3887:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

ATTTTTTAAT TTTCATGCAA ATTTTAAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60
 35 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACCTAGT CGAAAATAAA 120
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 300
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAACT 360
 45 TACTACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

(2) INFORMATION FOR SEQ ID NO: 3888:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60
 GTCTAGTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTCGATTCA TAAAATTAAA 180
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTCACACA GCTTCATTAA TAAAACGACT 300
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360
 AACGAATCCG CTTCATCCAA AATCAnCCAT TCTAACGCAC 400

(2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGCnAGA CGCATAcATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aAAGCAAGGC 60
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTTTnAAiT GCTGGAAAAT GTTAGCCTnC 480
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCcAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAnTGAAT TCGGACTACC 240
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300
 ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360
 10 GGTTTTGCnT CGCAAAACAT TTATTTTGn 389

(2) INFORMATION FOR SEQ ID NO: 3891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180
 TCTAGTGCCT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTCGAACC 240
 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300
 30 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360
 ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACcTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

(2) INFORMATION FOR SEQ ID NO: 3893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

| | | |
|----|--------------------------------------------------------------------|-----|
| 15 | GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT | 60 |
| | GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACCTGCT | 120 |
| | GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT | 180 |
| 20 | TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTGTAGAT | 240 |
| | CCAGGTCCAA CTGGTTTAGA AAAGAAAACCT TTATTATCTG AAGCTGAATT CAGAGATTAT | 300 |
| | TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAATGGG TGCCAGAAGG TCATTAAAAG | 360 |
| 25 | ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACCTnA | 400 |

(2) INFORMATION FOR SEQ ID NO: 3894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCTTG | 60 |
| 40 | ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT | 120 |
| | TAGTACGTGT ATATATCGTT CAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC | 180 |
| | GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCCTGA AGAAGATATG CCTTACTTAC | 240 |
| 45 | CAGATGGACG TCCGATCGAT ATCATGTAA ATCCTCTTGG TGTACCATCT CGTATGAACA | 300 |
| | TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG | 360 |
| | cATCACCAGT ATTTGaCGGT GCaAACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG | 420 |
| 50 | GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCCnTCCGA | 480 |
| | TAACC | 485 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

10 GAACAACATA CCTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTCTT 60
 AGATTGTGGT TTTTAGTTG GTGCCACTGc TTTAACCTTT TCATTGATTT CAATAACAGG 120
 15 TGTTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180
 TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCTGGTGTT GGCGGTGTTG GAGTTTCTGG 240
 CTCACCTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTTCC GGCTCACTTG GTACTTCTGG 300
 20 TGTGTTGGTGGc GTTGGTGTTT CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360
 CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTTGA CCTTCATTTT GGGCCGCTTA 420
 CTTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC 480
 25 TGGGGTTAAC CTTAAATTGG AACCTCC 507

(2) INFORMATION FOR SEQ ID NO: 3896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGGnGACTTG TGACAATCGC 60
 40 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG 180
 TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 45 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

| | | |
|----|--------------------------------------------------------------------|-----|
| | TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT | 60 |
| 10 | CAGAAACAGT TCGTCACATG GGTAAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC | 120 |
| | ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT | 180 |
| | CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA | 240 |
| 15 | CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC | 300 |
| | AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TCGGCACATG CTCCTATCAA | 360 |
| 20 | ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3898:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 400 base pairs |
| 25 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT | 60 |
| | GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA | 120 |
| 35 | TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTTG ATGAGGACTT AGCAACACGG | 180 |
| | GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA | 240 |
| | TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG | 300 |
| 40 | ACAAAAATGG TGTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG | 360 |
| | ATGTCGCGTC ATTTAAAnGGA AGCGATTCAC CATCGnGATC | 400 |

45 (2) INFORMATION FOR SEQ ID NO: 3899:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 400 base pairs |
| | (B) TYPE: nucleic acid |
| 50 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

55

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAATCGTTG 180
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300
 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360
 10 TTCTTGGAAT TGTGGACAAT CGGCTTGGA nTCTTTnCTC 400

(2) INFORMATION FOR SEQ ID NO: 3900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120
 TAATGTTATT TGTTCATTCA CTTTCATTCC AAACATACCA TCACATCCTC ATTCATTTTT 180
 CATATAATTC TGTAATTTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240
 30 TTTGTTGTCC TTCCCAACT TGCATTGCTT GTAGAATTTC TTTTCGAAAT TCTCTATGTT 300
 GGGGCCCCGn AACTTGCATT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360
 35 CATCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400

(2) INFORMATION FOR SEQ ID NO: 3901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60
 TTTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CAACTCAAT GCGGCTCATC 120
 50 GCATTCATTT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTTACCTT TTAATTTGGA CGGTTTAGAC 360
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240
 TTCTTTGTGT TTAATTTTAA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360
 AAGTTGGGCT ACCAaCGGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTTGGTGA TTTCAAATCA TGAGACTGGG 60
 ACAGAAATGA TGTTTTATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTTTGATG 120
 AACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180
 TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240
 ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360
 CTTTTTAGGT GGGTTTAGGG AATTTCCTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10 CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60
 TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG 120
 CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180
 15 AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240
 ATAGCATATC AGAAGGCACA CCCGGAGAnC TGAAACATCT TAGTACCCGG AGGAAGAGAA 300
 AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCCAA CCAnCAAGCT 360
 20 TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA 400

(2) INFORMATION FOR SEQ ID NO: 3905:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60
 35 TGgTAAATGA ACAAATCATT GATATTTTCAG GTCCGTAAAG GGGCGAAATA GAAGTGCCGG 120
 GCGATAAGTC AATGACACAC CGTGCAATCA TGTTGGCGTC GCTAGCTGAA GGTGTATCTA 180
 CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTTTCC gACTGTTAGG 240
 40 TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300
 TAACACGCCA CATCAAGTnT TGTnTACAGG TAATTCCGGG TACGACAACA CGATTGATAG 360
 TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

45

(2) INFORMATION FOR SEQ ID NO: 3906:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTCAGCAGT AGAAGAGGGA 60
 ACATTCTAAA CTAAATTTCG TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTc AAAAATGATA AAATCGACTT TATTTGGAGT 180
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAAGTGG GTTCTGTGAC ATTAACGTCT 240
 ACAAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300
 10 AACCATTAAc AGCGCCATTt AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360
 AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

25 AATTAGGTAA TTCAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120
 GGTCTCGTAG TGTAGCGrTT AACACGCCTG CCTGTCACGC AGAGATCGCG GGTTTCGATTC 180
 30 CCGTCGAGAC CGCCATTATT ATTACCATTa CGGTTcAGTA GCTCAGTTGG TAGAGCAATG 240
 GATTGAAGCT CCATGTGTcG GCAGTTCGAC TCTGTCCTGa ACCATTCTTA ATTCATGGCG 300
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTcGAGGG TTCGATCCCC 360
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420
 TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtcAmCCnGy TCCaTaATTT CnAAnAATTC 480
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

50 AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180
 AAAAGATATA GGGATTATAT TCGTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240
 5 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300
 TATCATCATT TGTGTTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

(2) INFORMATION FOR SEQ ID NO: 3909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180
 GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAGCG 300
 30 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCGTTCCCT AAAATTAATC CAGGGCTTAA 360
 CATTGCGAGT CCAGGTATTG GATCCAAGCT AATGGGGCCG 400

(2) INFORMATION FOR SEQ ID NO: 3910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAAGAGAA GGTACAGTAG 180
 50 CTGTAGTTGG TGACGTTATT GTTAAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAG

400

(2) INFORMATION FOR SEQ ID NO: 3911:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

| | | | | | | | | | | | | |
|--------|-------|---------|------|---------|------|--------|-------|--------|-------|---------|-------|-----|
| CGTGTA | CTC | AAGTTAT | GGG | TCCTGTA | AATT | GATGTT | CGAT | TTGAAC | CATAA | CGAATTC | CCTA | 60 |
| AAATTA | AATAA | CGCCTT | GGTT | ATTGAT | GTGC | CTAAAG | AAGA | AGGTAC | AATA | CAACTA | ACAT | 120 |
| TAGAAG | TTGC | GCTGCA | ATTA | GGTGAC | GACG | TTGTT | CGTAC | AATTGC | GATG | GATTCA | ACTG | 180 |
| ATGGT | GTCCA | AAGAGG | CATG | GATGTA | AAAG | ATACAG | GCAA | AGAAAT | TAGT | GTACCT | GTTG | 240 |
| GTGAC | GAAAC | ATTAGG | TCGT | GTATTT | AATG | TACTAG | GTTG | AACAAT | TGAC | CTTAA | AGAAG | 300 |
| AAATT | AGTGA | TTCTGT | TCGC | CGCGAT | CCTA | TCCAT | CGTT | AAGCAC | CAGC | ATTCC | GATGG | 360 |
| AACTTT | TCAA | CAGAAG | TTCC | AAATTT | TTAG | G | ACAGG | GTA | | | | 400 |

(2) INFORMATION FOR SEQ ID NO: 3912:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

| | | | | | | | | | | | | |
|---------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|--------|-----|
| TTGTACA | AGT | TGAAG | AAAAA | TCAAC | ACAAC | CAAAAG | GTAG | AAAATT | CAAA | GATTT | CACTA | 60 |
| GTAAATT | TTAA | TATAG | CATCA | GAAGC | TAAAG | AAAAT | GAACC | TATAT | CAGTC | ATTGG | TATC | 120 |
| CAAATC | CCTAA | TGGAA | AATAA | CTACA | AATGT | ATGAAT | CAAC | TGGTA | AAGTA | TTATC | AGTGA | 180 |
| ATGGGA | AATAT | AGTGT | CATCG | GATGCA | ATTA | TTCAG | CCTGG | TAGCT | CTGGT | TCACCT | TATAT | 240 |
| TAAAT | AGTAA | ACACGA | CGCT | ATTGG | TGTAA | TCTAT | GCCGG | TAATA | AGCCA | TCAGG | TGAAA | 300 |
| GCACC | GAGG | GATTT | GCTGT | TTATTT | CTCT | CCTGA | AATTA | AGAAAT | TCCA | TTGC | AGATAA | 360 |
| TTTAG | ATAAA | T | nATTA | AGAC | CT | nGAC | ATT | CACCCA | ATCC | | | 400 |

(2) INFORMATION FOR SEQ ID NO: 3913:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

| | | |
|----|--------------------------------------------------------------------|-----|
| | ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT | 60 |
| 10 | TTCAC TTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA | 120 |
| | AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT | 180 |
| | TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGA CTTGTGA | 240 |
| 15 | CAATCGCTTG CTTCTTTCCT CTTCTTCGGC TCTCGCTTAC TCATTTAGCT CTA CTAACT | 300 |
| | CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT | 360 |
| | CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

30

| | | |
|----|-------------------------------------------------------------------|-----|
| | TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT | 60 |
| | CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTTAAT | 120 |
| 35 | GCCAAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT | 180 |
| | CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT | 240 |
| | TCGGTCTAGT TGCTAAATAA TCTTTAGCTA ATTGAATTGC TGGTGTGCA GCATAACAAG | 300 |
| 40 | CTTCTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTTG | 360 |
| | nACAGCGGCT GCTTTACGAA TTCCAAC TGC TGATTCCAGT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3915:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

55

TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180
 5 TCGAAATTGA ACGAnAATTC AAAAACATTA TATCGTGACT TAGTTGAAGA AAAAATAATA 240
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300
 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360
 10 ATTAGAAACA G 371

(2) INFORMATION FOR SEQ ID NO: 3916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAAATAGC 60
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180
 GACTAATAGT AAAAAGTTA ATCACAAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300
 AGAGCTTGAT TTAAATTGA GAAACAAC TATTGAAAAA CAGATCTTTA CGGTAACATG 360
 GGTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

(2) INFORMATION FOR SEQ ID NO: 3917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCCnTGAAG GAATAACAaC CTTTAGACCT 60
 GGAGATTGAG CTAAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180
 GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTGG TAGTCCTTCA 360
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60
 TCGGGTCAAC GCCTACTGCC TTAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120
 CTTTCACTTT ATCTCCAGAC ATTAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180
 ATGTTCTGCT AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240
 CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300
 GGTCCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360
 CCGACCATCA CGGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAACTG 120
 CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTTG 180
 GTAAAACTGC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300
 ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnc TTCACAAATG 360
 CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG | 60 |
| | AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC | 120 |
| | ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA | 180 |
| 15 | ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT | 240 |
| | CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG | 300 |
| | GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA | 360 |
| 20 | GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3921:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT | 60 |
| 35 | TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA | 120 |
| | AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT | 180 |
| | CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA | 240 |
| 40 | ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG | 300 |
| | GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG | 360 |
| 45 | TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3922:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

GTGCGCTCTA ACCAGCTGAG CTATAGGCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180
 CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC GGCTTCGGGT 240
 GTTACAAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300
 10 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTTGn 400

(2) INFORMATION FOR SEQ ID NO: 3923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120
 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGCCACT 180
 30 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300
 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360
 35 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60
 CTTCAAAC TA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTTCCT ATCATATAAA TGATAGATTC AAATAGATTT 300
 GTAGGGTTGT CATGCCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AAnTCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTCG AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTCGCTACC CCTCCAGCTT ATTCATATAA 180
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG 240
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300
 GTGTTACCGC CGTGaAAGGG CGTGtgCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAAnTGAAT TCGGACTGAC 480
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

400

(2) INFORMATION FOR SEQ ID NO: 3927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT | 60 |
| | GGTTGCATTT AGCGCAACAT GACCATAGTT TTACTAAAGC ACAGCGCGCA AGTGATTAAA | 120 |
| | GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT | 180 |
| 20 | CAGGAAGACT ACCAAGCTTA TGTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT | 240 |
| | ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT | 300 |
| | GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGGG TGAGTTTAAG TCCATCGCTA | 360 |
| 25 | AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

| | | |
|----|--------------------------------------------------------------------|-----|
| | GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTGTGTC | 60 |
| 40 | AnTTTGTAA ATATAGGCCG TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA | 120 |
| | GTAATACATC TCCAACATTT GCCTTTAATT CTTTGGCGAT GACTACCGGT CCTGGATGTG | 180 |
| | GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA | 240 |
| 45 | CTGAAACATT TGC CGTTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA | 300 |
| | CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA | 360 |
| 50 | CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTAAA CGCTGTTATC TTTATGCCAG | 60 |
| 10 | TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG | 120 |
| | TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG | 180 |
| | AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA | 240 |
| 15 | CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA | 300 |
| | TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT | 360 |
| | ATTCACCTAC CACGnAAATT ATAGGTGTTG AACCCnAGT | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

30

| | | |
|----|--------------------------------------------------------------------|-----|
| | ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT | 60 |
| | CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCAAATGA TACATCGAAT | 120 |
| 35 | GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAAGCA GCAAGAAAAT | 180 |
| | GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA | 240 |
| | AAAAATAAAT GAATAAGTAA GGTTCACACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT | 300 |
| 40 | TGTCGTTGTG CCAAATTTGA ACGnTTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT | 360 |
| | ATTATTTCCA TGnA | 374 |

(2) INFORMATION FOR SEQ ID NO: 3931:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

55

TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120
 TTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240
 GTGTATTGTA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300
 AACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTTAAAATGC 360
 10 CATTTAAATT CTAGGTGTTT CCnTAnC 387

(2) INFORMATION FOR SEQ ID NO: 3932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG 60
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120
 TGACCGATAG TGAACCGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

(2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60
 CTTTTTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120
 AGCTTAACTT CTGTGTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180
 ATATGAATGT AAATTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTTAT TTCGTTCGnT 60
 CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTGGGGCC 120
 CCGCCAACCTT GCCATTGTCT GTAGAAATTG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180
 CCCCACCTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240
 AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300
 TTGAAAAGAG CGTGTTACAC GGGCATTGTT TTACAGTCAA CTA CTGCTAA AATAAAATTA 360
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG | 60 |
| | TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGG AGAACCTAAA | 120 |
| | AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT | 180 |
| 15 | GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC | 240 |
| | TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA | 300 |
| | TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT | 360 |
| 20 | TTACAGTCCG CCGCGTTTAG CACTTCGCTA CCCTCCAGCT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3937:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

| | | |
|----|--------------------------------------------------------------------|-----|
| | GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC | 60 |
| 35 | CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA | 120 |
| | TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAgT | 180 |
| | GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCTTC AGCCGCCCCA | 240 |
| 40 | TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAAACC TCAGCCTTCC AAGCTGATGT | 300 |
| | TGTGGGTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG | 360 |
| 45 | GTAGAGCTAT CGGCTGTTAA CCGATCGGTC GTAGGTTCGA GTCCTACCTG TGGAGCCATG | 420 |
| | GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC | 480 |
| | CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA | 540 |
| 50 | TkGTTGgAGG aAGtTGTCcCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT | 600 |
| | CACAAGCTT | 609 |

(2) INFORMATION FOR SEQ ID NO: 3938:

55

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGGAAATCGCT | 60 |
| | AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTAACA CACCGCCCGT | 120 |
| | CACACCACGA GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT | 180 |
| 15 | CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG | 240 |
| | CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC | 300 |
| | GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA | 360 |
| 20 | GnGGTTAnAG CGCACCCCTGA TnAACGTGAA GTCGGTGgTT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3939:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

| | | |
|----|--------------------------------------------------------------------|-----|
| | AGTTTTGAAT GTATAAATTA CATTCAATATG TCTGGTGACT ATAGCAAGGA GGTCCACCTG | 60 |
| 35 | TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC | 120 |
| | CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA | 180 |
| | TCGGCTGTTA ACCGATCGGT CGTAGGTTTCG AGTCCTACCT GTGGAGCCAT GGCTCTTGGT | 240 |
| 40 | CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTTCGAGTC CCGTAGAGTT | 300 |
| | CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC | 360 |
| 45 | GGTTTCGAAC CCTnCATTTT CCACCATTTG GTTATTAAAn | 400 |

(2) INFORMATION FOR SEQ ID NO: 3940:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

ACACAACAGC TGTTTCAAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300
 10 AAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

(2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120
 25 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180
 GGTCAATCAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300
 30 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360
 AAAAATTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120
 50 CATTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTnAT 300
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360
 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300
 CGCCTTATAT AGTTTGTAAG TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360
 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60
 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120
 GCAACCCGTT GACCATTGCC CACACCATTG GATAGGAGCA TGTGCGCAAT GGCATCCACA 180
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGACTAGCGC AACATGATTA 240
 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300
 GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGA 360
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATAtC AATCAn 406

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTCGAAT 60
 AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT 120
 TTAAAGGAAA TTCAAGAAGA TGTTCTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT 180
 GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT 240
 CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA 300
 GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA 360
 ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3946:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGThT TAATAGGnTC TGAAACGATA 60
 CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT 120
 GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC 180
 CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCCGG 240
 CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC 300
 GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC 360
 CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT 400

(2) INFORMATION FOR SEQ ID NO: 3947:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCCGGCCAGA GGACTTGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC 120
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180
 10 GGCAACGTTC TACTCTAGCG GAAnTAATTC GnACTACCAT CGACGCTAAG GAGCTTAACT 240
 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300
 TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGChTTCG CAAAACATTT 360
 15 A 361

(2) INFORMATION FOR SEQ ID NO: 3948:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120
 ATAAAGC3GA TTTCGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180
 ATTACTATAT TTAAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGCnGA ATAGGCCACC 360
 GATACATCAC CAACAATTGG nA 382

(2) INFORMATION FOR SEQ ID NO: 3949:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

55

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG 300
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGn CTCAATGnGG 360
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGGTTTT GCTTGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA 120
 AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAACT CTCGTGGTGT GACGGGCGGT 360
 30 GTGTACAAGA CCCGGGAACG nATTCAACCG 389

(2) INFORMATION FOR SEQ ID NO: 3951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTTGAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60
 TTACCAATTT TAAATGAATT TAATAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT 120
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTC TATTACTCTG 180
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240
 GGTTCAACTG GAAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300
 AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

(2) INFORMATION FOR SEQ ID NO: 3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATATA AGTTGTTCT CAGTTCGGAT 60
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCGTC ACACCACGAG AGTTTGTAAC 180
 ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240
 GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360
 GntTTTGAAT GTTnnTTAA CATTnCAAAA AAATGGGGCC 400

(2) INFORMATION FOR SEQ ID NO: 3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240
 TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

5 AACTACATA ATGAAAATGC CGTTTTAATC GGTAATTAA ATATGGATGA GTTTGCAATG 60
 GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTTGA CCATAAAGCA 120
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATT 180
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA 300
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360
 15 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 3955:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

25 TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTC 60
 GGTCCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180
 CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTTATT CTACAAAAGG CACGCCATCA 240
 CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300
 35 TCCGGGGGTG CTTTTCACTT TTCnCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360
 TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3956:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

50 GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

55

ATAAAAATGG AGCAGAAGAC GGGATTGCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240
 5 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAn 400

(2) INFORMATION FOR SEQ ID NO: 3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120
 25 AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240
 TTTTGGGGTG CATATTTTGT ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG 300
 30 ACCTGAGACA GGACTTACAC AGCCTGGChA GACCATCCGT nTGTGGGTGA CTCTCACACA 360
 GCCACACATG GnGCCTTTT 379

(2) INFORMATION FOR SEQ ID NO: 3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA 60
 ATATATTCAA GGTCAGAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120
 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAAACAG CAGTAAGATA 180
 50 ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

AATAAGACAT TTGnCCAAC TGA CACTACC ATTAAAACT

400

(2) INFORMATION FOR SEQ ID NO: 3959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

15 GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTATCAAA AACACAGGTC TCTGCTAAAC 60
 CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTAA GAGGAGTGGT 120
 TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180
 20 CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240
 GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300
 25 CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360
 CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

40 TGGTCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60
 TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180
 45 ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240
 ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300
 CGCTGGAAC TTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCCA CGCCGTAGGC 360
 50 TTAAGATTCC TGAAGTCTAG TCGTCTGGC CAATTTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT | 60 |
| 10 | AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC | 120 |
| | GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG | 180 |
| | GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC | 240 |
| 15 | AGTAAATGTG GAGCCGTAGC GAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA | 300 |
| | GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG | 360 |
| 20 | GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACCTG | 400 |

(2) INFORMATION FOR SEQ ID NO: 3962:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 361 base pairs |
| 25 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

| | | |
|----|---------------------------------------------------------------------|-----|
| | TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC | 60 |
| | AAGTGCTCTA CCAAGCTGAG CTA CTCTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC | 120 |
| 35 | CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG | 180 |
| | TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA | 240 |
| 40 | TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG | 300 |
| | ACGGGATTCTG AACCCGCGAC CCAACCTTG GCAAGGTTGT ATTCTACCGC TGA ACTACTT | 360 |
| | C | 361 |

45

(2) INFORMATION FOR SEQ ID NO: 3963:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 375 base pairs |
| | (B) TYPE: nucleic acid |
| 50 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

AAGTGTCTTA TTTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAAT 120
 GCGGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180
 5 AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240
 ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300
 ATATTCACTA TCAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360
 10 TTGGAATATA TTTAT 375

(2) INFORMATION FOR SEQ ID NO: 3964:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA 60
 25 ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTTGTACAA TTAATGTGAC ATGACTAGGT 120
 CTTGCACGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTCGTT ATGATTTAAT 180
 30 ACGCCTAATT CTTTCATTTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360
 35 ACCATTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

(2) INFORMATION FOR SEQ ID NO: 3965:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT 60
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAACCTAC CATTGCTTGT 120
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180
 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA 240
 55

TCAGCACCTG CTTTAGGTTC CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360
 TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

5 (2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60
 TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120
 20 GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180
 AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240
 AAAGTATTTT AAAGTAAAAT TACATGTTAA TACGTATaTA ATGGcGAGAC TCCTGAGGGA 300
 25 GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG 360
 AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

30 (2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

40 GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60
 TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120
 45 AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180
 TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAACT GGTATCGGCG 240
 AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300
 50 GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360
 TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

55

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | ACCCCGGCAC TATAAAAATG GAGCAGAAGA CGGGATTCTGA ACCCGCGACC CCAACCTTGG | 60 |
| | CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC | 120 |
| | CACGCCGTAA nCTGAGGATC CTAAGTCTAG TCGGTCTGCC AATTCGCGCA CACCCGCAAA | 180 |
| 15 | TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC | 240 |
| | AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT | 300 |
| | GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT | 360 |
| 20 | GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3969:

| | |
|----|-------------------------------|
| 25 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 400 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG | 60 |
| 35 | CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT | 120 |
| | TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG | 180 |
| | GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG | 240 |
| 40 | ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT | 300 |
| | CATGTATTCC TATTTTAAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA | 360 |
| 45 | ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC | 400 |

(2) INFORMATION FOR SEQ ID NO: 3970:

| | |
|----|-------------------------------|
| 50 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 419 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

55

GATAAGATCA GCCGAAAATG GATGGTGTGA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60
 TTTTAAATGG CATTGTGTAC GACACCATTA CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120
 5 CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTGCGA GTGCAGAGGC GCCACTGAKA 180
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240
 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300
 10 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTTnCA ATGTCTAAT 419

(2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT 60
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120
 30 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300
 35 CACCAACACT AAAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360
 GGGTTTCCAn AGTCCGTTAT G 381

(2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCTG 120
 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60
 20 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180
 TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCTTGGA 240
 25 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300
 TTGTTTCTGC TTCATATTTT GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGAGTCTAA ATCAAAGTTG ATTAATAAAT 120
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAAACT 300
 TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360
 CACTTGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GGCGACCGCC CCAGTCAAAC TGCCCGCCTG 60
 ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA 120
 TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT 180
 ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC 240
 TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC 300
 AGTGCCCAA TCGTTAACGC CTTTCGTGCG GGTGCGAACT TACCCGACAA GGAnTTTCGC 360
 TAACTTAGGA CC 372

(2) INFORMATION FOR SEQ ID NO: 3976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 CCCATTTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA 240
 ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCAATTATT 300
 TTAAAGCTCA TTTACATAAG TAAACTCTGC TTTAAATGAT TTAATCATT GTCTGCTAAA 360
 ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn 395

(2) INFORMATION FOR SEQ ID NO: 3977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

5 TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60
 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180
 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 240
 10 GGAGCAGAAG ACGGGATTTCG AACCCGCGAC CCAACCTTG GCAAGTTGTT ATTCTACCGC 300
 TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360
 15 CTTAAGTCTA AGTGCGTCTG GCCAATTTC GCCAnACCCG 400

(2) INFORMATION FOR SEQ ID NO: 3978:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120
 CTTTGGTTA CAGAAATTC AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240
 35 AGCTCTAAAA GTTGTATTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300
 GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360
 GGATTCCGAA CCTCGGACCC TCnGAnT 387

(2) INFORMATION FOR SEQ ID NO: 3979:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

50 TGGAGCAGAA GACGGGATTC GAACCCGCGA CCAACCTT GGCAAGGTTG TATTCTACCG 60
 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120
 55

CGAACCTCTG GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300
 5 ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCATTTG 60
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTTGGCC AAGCATACAA GCCGGCATTT 120
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA 180
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTAATTACCG TTTTGGCAGA 240
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACTTAGT TCAAGGTACG CAGAACATCT 300
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360
 30 nGTCAGCCGT TTTAATACGA GGATGTTCCG CTAnGTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

45 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120
 CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240
 GGATTTTACA GTTGTCGCAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAT 300
 GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 60
 TAATGTTTCA ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAGCAAA 120
 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTC 180
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240
 TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300
 AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA 360
 AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

(2) INFORMATION FOR SEQ ID NO: 3983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60
 AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120
 TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG 180
 CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT 240
 AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT 300
 TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360
 GTTACTAACG ACGATATGCC TTGGGGGAGC 390

(2) INFORMATION FOR SEQ ID NO: 3984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120
 10 CGTTTCTTTT ATCCATTICA ATATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GCGGTTCTAA 240
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3985:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAC TAAAGAAATT 60
 ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTAG AGGCTGGGAC ATAAATCCCT 120
 AAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT 180
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATTT 300
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

(2) INFORMATION FOR SEQ ID NO: 3986:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCTTATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATTA 180
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCGGT GCGGGAACGA 240
 5 TTTTGATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60
 CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180
 TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240
 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG GGGACTAnCG 300
 30 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60
 ATGTTCGCCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG 180
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGAATCCTAG GCGGTGAACG ACCATCCAAA 300

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

(2) INFORMATION FOR SEQ ID NO: 3989:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15

| | |
|-------------------------------------------------------------------|-----|
| CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA | 60 |
| ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA | 120 |
| GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG | 180 |
| CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC | 240 |
| ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG | 300 |
| AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCGTC GGAATCTGGG AGGACCATCT | 360 |
| CCT | 363 |

25

(2) INFORMATION FOR SEQ ID NO: 3990:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

40

| | |
|-------------------------------------------------------------------|-----|
| TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTCTTACTT CTTTATCGTG | 60 |
| GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTAATTTCTA GGATCGACCA | 120 |
| ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT | 180 |
| ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAAATGC | 240 |
| CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT | 300 |
| CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT | 360 |
| CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT | 400 |

50

(2) INFORMATION FOR SEQ ID NO: 3991:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA | 60 |
| 10 | GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT | 120 |
| | TCTTTTGGTT ACAGAAATTT CAACAACTTT AAAGCAnGTA TAATGATGAT TTTCAGCTTG | 180 |
| | TACAAAGGAG AAAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn | 240 |
| 15 | GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTGTT | 300 |
| | GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG | 360 |
| | ATTCGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCATTATT ATTACCGTTA TTGTATTAGT | 60 |
| | CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTnGACA | 120 |
| 35 | TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT | 180 |
| | AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA | 240 |
| | CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTAAAAG AATTAGCTAA | 300 |
| 40 | AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT | 360 |
| | TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

55

TTATCAGAAG AACAAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GGNGCATTAC CCGTTGGATT ATTACCGAAT 180
 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC 240
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300
 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT 360
 CCGCCGGCAT TGAGAGCCTT AGA 383

(2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60
 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180
 GCACCGGGCA GCGGTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240
 GATAAACAGT CGCTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTGAAAGAGC 300
 ACCCCTTCTC CCGAATTACG GGGTCATTTG CCGATTCTT AACGAGATTC GCTCGCTCAC 360
 CTTAGA 366

(2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60
 TTCATTAAAA GCAACGTTAT GntGAATCGG ATAGAGGCAT CTACTGGGAA ACGATTACAA 120
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC 240

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG 359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA | 60 |
| | ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA | 120 |
| | TTTAACACAT AGTAAGAAAA ACACTCATAA ATTGATTCT AATTGAAATC ATCTTATGAC | 180 |
| 20 | TGCTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA | 240 |
| | AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTAA GACATAAAAA AAGAGACCTT | 300 |
| | GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTGCCTG GGCAACGTTC TACTCTAGGC | 360 |
| 25 | GGAAnGTAAG TGGGACTTAC CATCGACGGn TAAGGGGCTT | 400 |

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT | 60 |
| 40 | GTCAnGCGGG CAGTTTGACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG | 120 |
| | TTCCCTCAGA TGTTTGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCC | 180 |
| | AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA | 240 |
| 45 | GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG | 300 |
| | TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCGnCTCA TCGCATCCTG GGGCTGTA | 358 |

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAACATTA TTTCCTGAAG 60
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTC CAACAAGTAG 120
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG AATTAAATTA TTTTAACAT CCATTACTTT 240
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTTC ATGTCTTACC 300
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCACCAA GGTTAGGGCA 360
 15 TAACACTTTC TATTTCGGAG GTAGCAAAGA CAAATTGCGA 400

(2) INFORMATION FOR SEQ ID NO: 3999:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCTTAG TGCTGCACTA ACGCATTAA GACTCCGsCT GGGGAGTACG ACCGCAAGTg 60
 30 AAACCTCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120
 AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180
 CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT 240
 35 GGGTTAAGTC CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATT AATTGGGCAC 300
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC 360
 40 CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

(2) INFORMATION FOR SEQ ID NO: 4000:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAA GGTTAGTTTG 60

55

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240
5 ATTTGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAAGT ACATGsCAA aGtTTATGAT 300
GATTACmAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360
TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60
CTTAACTTCT TGTTTTTCCG ATGACAGCTT CTATTTAGAG AATGTCATGA TTATTTTATA 120
25 TTCACCTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180
AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTCAATAA GTGTTTTCTC AATTTAAAAT 300
30 CAAGTTCTTT CAAGGAAATC TGTTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360
TTGTACCGTA TnATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60
GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120
TTATGCATAC AGATCCAATG AAATTCTTAC CTGAAGATGG TAGCTTGCAAG TTAAGTCTG 180
50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240
CAATGCAGCG TATTGCACTG GCTAACAAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

(2) INFORMATION FOR SEQ ID NO: 4003:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

| | | |
|----|-------------------------------------------------------------------|-----|
| 5 | AGAAATATAT GCATTTGCGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG | 60 |
| 10 | ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA | 120 |
| 15 | CGACAGGTGA TGGGGTTGAA AGTGTAACGn GCTACACTGG TCATGATGCT GCTAAACTAC | 180 |
| 20 | GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG | 240 |
| 25 | TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT | 300 |
| | GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAACAC ATGATTTAAC | 360 |
| | AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4004:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC | 60 |
| 40 | GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTAAAG CAGTAAATGT | 120 |
| | GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC | 180 |
| | AGGTGATCTA CCCTTGGTCA GGTGGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA | 240 |
| 45 | CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG | 300 |
| | AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA | 360 |
| 50 | nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG | 400 |

(2) INFORMATION FOR SEQ ID NO: 4005:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC | 60 |
| 10 | GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC | 120 |
| | ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTA | 180 |
| | TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT | 240 |
| 15 | GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG | 300 |
| | ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA | 360 |
| 20 | TGTTGCCTAA TTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC | 415 |

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 444 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

| | | |
|----|--------------------------------------------------------------------|-----|
| | CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG | 60 |
| 35 | ACATTGTGTC TTCGAGTCGT TGATTTCAACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA | 120 |
| | GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG | 180 |
| | AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACCTT CGGGAGAAGG GGtGCTCTTT | 240 |
| 40 | AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC | 300 |
| | AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT | 360 |
| | TAAhGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC | 420 |
| 45 | CGTAACTATA ACnGTCCTAA GGTA | 444 |

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

TTTGAAGTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120
 TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT 180
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240
 CGTGCCGAAC TGGAAGTTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300
 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360
 GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC AAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120
 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG 180
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300
 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120
 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

(2) INFORMATION FOR SEQ ID NO: 4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTACTAAATG GTATTTATTC ATCGAGTTAC 60
 20 ATCTATAGTT TATTAAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240
 25 TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

(2) INFORMATION FOR SEQ ID NO: 4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60
 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGACTGG CACTGCTCCC TCAGGAGTCT 120
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT 240
 50 TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

(2) INFORMATION FOR SEQ ID NO: 4012:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

| | | |
|----|---------------------------------------------------------------------|-----|
| 15 | TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA | 60 |
| | AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTT TACTCTAGCG GAAGTAATTG | 120 |
| | GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTC | 180 |
| 20 | CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT TCTCGTTTCG | 240 |
| | TCAGATTCAA ACGTTTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG | 300 |
| | ACGTTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT | 360 |
| 25 | TTTTGGCCTG GGCAACGTTT TnATnCCAGC GGAAnTnAAT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4013:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

| | | |
|----|-------------------------------------------------------------------|-----|
| 40 | CGAACTGCCG AACCCGAAGA GCGGATTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC | 60 |
| | TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC | 120 |
| | GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT | 180 |
| 45 | CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA | 240 |
| | AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG | 300 |
| | CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG | 360 |
| 50 | AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC | 400 |

(2) INFORMATION FOR SEQ ID NO: 4014:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATTAGGACCT CAAGACGATA TTACTAAATT TGAATACTTA AAAAAATCTT CTCAAATAC | 60 |
| 10 | AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA | 120 |
| | CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC | 180 |
| | ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT | 240 |
| 15 | CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC | 300 |
| | ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA | 360 |
| 20 | nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| | (A) LENGTH: 377 base pairs |
| 25 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC | 60 |
| | ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC | 120 |
| 35 | ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT | 180 |
| | AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC | 240 |
| | GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCGAAC | 300 |
| 40 | TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG | 360 |
| | CCAGnTTATT CATATGA | 377 |

45

(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| | (A) LENGTH: 400 base pairs |
| | (B) TYPE: nucleic acid |
| 50 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

ATGACGCACC TGACATCCTC TCGGTTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180
 5 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240
 CTCTGTACAT TTTTTCCTCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATTGA 300
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTACGG 360
 GTGAAAAATA CGGTGTGTAG AaGTCGTGGT TTTTnAAATA 400

(2) INFORMATION FOR SEQ ID NO: 4017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAACCTG CCCGnCTGAC 60
 25 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180
 30 AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCTGT 240
 CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTACCC GAGTCTCTCG TTGAGACAGT 300
 GCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAACTTAC CCGACAAGGA ATTTCGTTAC 360
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAG ATCGAGCGGC 60
 50 ATATGAGGCA CGCCAAGCGA TTCAAACAT TAATGAAAAC AGTCCGCCAA TATTAATTGT 120
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360
 TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60
 TTGGGCTGTT CGCCCATTAAG AGCGGTACCA AGCTGGGTTC AGAACGTCGT GAGACAGTTC 120
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCCTTAGT ACGAGAGGAC 180
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60
 AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120
 GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180
 ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240
 TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300
 TTTGTTAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360
 TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTACGGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

(A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG | 60 |
| | CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG | 120 |
| | TTTGCAAGTn TAAAAGATCG TCCATTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA | 180 |
| 15 | GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCTTTT AATGGTTGCA | 240 |
| | GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT | 300 |
| | TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTTCATCAnT | 360 |
| 20 | AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT | 396 |

(2) INFORMATION FOR SEQ ID NO: 4022:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA | 60 |
| 35 | TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT | 120 |
| | AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT | 180 |
| | ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTTAG | 240 |
| 40 | CAGTAGTTGA CTGTAAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC | 300 |
| | CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA | 360 |
| 45 | ACACAGAGGC TGGCGG | 376 |

(2) INFORMATION FOR SEQ ID NO: 4023:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

CAAATGGTGG AGCCATAGGA GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcnGGCCAG AGGACTTGAA CCCCCAACCT 120
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180
 GGTGGAGAGT GACGGGTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240
 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT TACTCTAGCG GAA_nTAATTC 300
 10 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA 360
 CTCCTTGCTA TATCACCAGA C 381

15 (2) INFORMATION FOR SEQ ID NO: 4024:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

25 GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120
 TACATGAAGC TGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180
 30 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300
 AACAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360
 35 ATTTTCG_nAA CATC_nTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60
 50 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTGA GTCGGGTCCT AAGCTGAGGC 120
 CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

55

GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300
 GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

5 (2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

15 TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60
 CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120
 20 TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180
 TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240
 AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300
 25 AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGTGnG 360
 TGTTCTTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

40 TCATGTTTCG CTTGGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60
 ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTTCAGT 120
 TCTGCTTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180
 45 ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTTAGA CGTTACTAAT TGGCTATTAT 240
 CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300
 AGTTAGTGCG TGCAGAAACT TGTTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360
 50 GCCTCCGTTT TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

55

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180
 15 TTCAAACGTT TTTCACTTCGC CAAGCCATTT TTCTTTGTGT TTTACTTTTAA TTTTGACGTT 240
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 4029:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC CCTCTGCTTG 120
 TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180
 TACTCTAGCG GAAnTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA 300
 CATTCAAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

45

(2) INFORMATION FOR SEQ ID NO: 4030:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTTGTTTCT 120
 5 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240
 TTTGAACGCC ATATAAATAA TGATTTTGGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300
 10 CAAATTGTGG TTTGTnTTGG ATTTCAChTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360
 TGAATCTATA CCCTGCATCT TGTAGCnTCC 390

(2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

TGGTTCGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60
 CAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT 180
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240
 GAGGTATAGG TGTAATCCT ATCTTCCGCT CCATAATTTA ATATTTGCGG GGAGTAGTTC 300
 35 CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGCnC 360
 CATAATGCCT TCCAAAGGGG AATTTTTTGG TTnACCATT 400

(2) INFORMATION FOR SEQ ID NO: 4032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

GTATCGATGA GTTCTTCGG TCGTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60
 ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120
 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300
AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360
5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTT TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60
20 ACCGACTACA GCCCCcAGGA TCGGATGAGC CGACATCGAG GTGCCAAAct CCCCGTCGAT 120
GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCGGGGTA GCTTTTATCC GTTGAGCGAT 180
GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240
25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300
AGGGAACCTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCCAGTC AACTGGCCG 360
30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60
45 TTTCTGGTCT GTAAGTACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120
CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180
CTGCAGCTAA CGCATTAAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA 240
50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTTCGAA CAACGCAGAG 300
AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360
CAAATGACAG TGGTGCanGT TGTCTCACT CGTGTCGTGA 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120
 ATGTCACTTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180
 CATTAACTACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300
 CCTGTTTTTG GATTATGAA GGCTATTTGG GGTTCACCTCG AATGTCAGTT CGAGGAATAA 360
 TnAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT 400

(2) INFORMATION FOR SEQ ID NO: 4036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180
 CATTCTTCTA TCGATTTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAATG GCTATTGCAC GTACAAAGGC 360
 TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60
 5 TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTCTCGTT TCGTCAGATT 120
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTCGCCT 240
 10 GGCAACGTTT TACTCTAGCG GAAATAAATT GGGCTACCAT CGACGCTAAG AACCTTTCCT 300
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360
 15 TACnAAACTC GTTGCCTCT T 381

(2) INFORMATION FOR SEQ ID NO: 4038:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60
 TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTTAC TGTCATCGTA AAATGCAGCT 120
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180
 AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT 240
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300
 ATGAATGCTT TnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

(2) INFORMATION FOR SEQ ID NO: 4039:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

50 AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60
 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120
 CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

55

GAAGTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300
 CTAAGTCTAG TCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC 360
 5 GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTCTTGAC TTGTGACAAT CGCTTGCTTC TTCTCTCTCC TTCGGCTCTC GCTTACTCAT 60
 20 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120
 TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTtagac ATAAAAAAG 180
 AGACCTCAG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240
 25 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300
 GGCTCTCGCh TACTCATTTA GCTChACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360
 30 AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60
 GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT 120
 45 GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180
 TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240
 50 CTATCGATT ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300
 CTGTATCACC ATCCATCATA CGATTCAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360
 TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AACTGGTAA CACACCAGAC GGACGTAAAG 60
 CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120
 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180
 ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300
 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360
 ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA 60
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120
 AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT 180
 TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCTACTG GATAATAGC GAGGCTACCA 60
 TGTGTTTCA TCGTAGCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240
 TCTTTTGTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360
 15 CnTTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120
 CATTTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAATGAT TAATTGCACA 180
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGTnG 300
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGnAAGT 360
 GGTGCGATAC TTTGGGGCAT CGCTGTGGGG TAGGGGGnCh 400

(2) INFORMATION FOR SEQ ID NO: 4046:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

50 CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300
 5 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACnACn GGATTCTGAG 360
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

20 ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60
 TTACGTTTCAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120
 GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180
 25 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TCGGACATTA 240
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300
 30 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360
 GAATTTGACG GnGGACCAAG ATGcnTGTTT CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

45 CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGA CTCAGAT 120
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180
 50 GTACTAGTTG CCCC GCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTA ACTGT 300
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

(2) INFORMATION FOR SEQ ID NO: 4049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60
 GACACTACCT TCCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTCa CAACATTGTA 180
 ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240
 GCTATATGAT TAntATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300
 ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360
 CCCATACCGG GGTCATCGTC CAATACACGT TCCAAnCTnC 400

(2) INFORMATION FOR SEQ ID NO: 4050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCTG 60
 GTAACCCGAG AGGGGCCCTT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120
 GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCGGTCC TCCATTCAGT 240
 GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300
 CTAAACGCCT ATTCAGCTCG nTTCGTACGG CTCCACATTT ACTGCTAAnC TTGCATCAAT 360
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTG TTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120
 CCATTCGTTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCTAATC 180
 10 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300
 15 CCAACATGTG GGnTCCGGTT CATTGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180
 35 TTCCCCATTC GGAAATCTCT GGATCAAAGC TTA CTTACAG CTCCCCAAAG CATATCGTCG 240
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300
 TTAATCnATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360
 40 TTCATTAATT TTAAATGGCn CAATTTAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300
 AAAAGCAGAA TTAATTGATC AAAGTCGGT ACTTCATTGA GCCACAAGAT TTATTTCAGTG 360
 CGATGATCGT GAAATTGAA CGCAGGATTT CCGATATAGA 400

(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTCCTACAG 180
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240
 TACCTGCAAA TGCATATCCG CAAAATATCG TTACTAATAT TTGGGhCATA CTCATCATAC 300
 30 CACCCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

(2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAACTACT TCTACTTGTT 60
 CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTCAC 240
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

(2) INFORMATION FOR SEQ ID NO: 4056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTTGGTTT ACTTCATGTT GAGTTT TAGA CATTTTAACC ATCTCCAATA TAAAAATAAA 60
 TTAAATTAAA TTCTCAGGGA CTTGCATGAC GCCACCTGTA TTTGCGCTAG TTACTAGGGC 120
 AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG 180
 GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTG TTAAATCAAT 240
 AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA 300
 AATATGaCCA ACTGcAATAC CTCTTGTTGGc ACCGGtAAAA ACGCCCATCA GTkAATTAAT 360
 GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATT TTCAGG 420
 nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT 480
 G 481

(2) INFORMATION FOR SEQ ID NO: 4057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTGCCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG 60
 ACCTTTCTTG ACTTG TGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC 120
 ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA 180
 CTTGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTA GACATAAAAA 240
 AAAGAGACCT TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT 300
 ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA 360
 ATCGGCTGcn TCTGTnCCT 379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120
 TTTAAAGGCT AAACCTACCAA TGTTTTCAAT GGATTTCCTAA AATGAATCAT CTGGGATGAC 180
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTCATT AAATGTTGAT ACACCATTTC 300
 AATACCATTTC TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360
 GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTCGTCA GCTCCACATG 240
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360
 ATCCCGT 367

(2) INFORMATION FOR SEQ ID NO: 4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

5 TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTCAG ACACCGCATT 60
 CAGATTCAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120
 GATTCAGATA GCGATTCAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA 180
 10 GACAGTGATT CGGATTCAGC GAGTGATTCT GATTCAGATA GTGATTCCGA CTCCGACAGT 240
 GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTCAGA TAGCGATTCT 300
 GACTCAGATA GCGATTCAGA ATCAGACAGC GATTCAGATT CAGACAGCGA CTCAGACAGT 360
 15 GACTCAGATT CAGA 374

(2) INFORMATION FOR SEQ ID NO: 4061:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60
 30 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCACGAT ATTCATCTAA 120
 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180
 TTAAATAGA TTTTAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtKGTtG ATTTCGTTAT GATTTAATAC 300
 GCCTAAWTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTAGCCA AGAAATTCAA 420
 40 ACCATGTTTA CC 432

(2) INFORMATION FOR SEQ ID NO: 4062:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

55 TATCTTCGTT CTCAATAGAA TGATTTAAAC CTTGATTTT TTTATCTAAA TGAATACCAA 60

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTTCGT 180
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGANTCA 300
 ATTAACGCAT CAGTATTAGG GANTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360
 nTTGGATTTG GAGCTAACCA CATCCA 386

10 (2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC ACGTAGGGCG 180
 ATGGATAACA GGTGATATT CCTGTACCAC CTATGAATCG TTTAATCGA TGGGGGGACG 240
 CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360
 CGAGTTCGTT GGnTTTCACA ATGGCC 386

35 (2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC 60
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240
 AGTCTTCGAT CGANTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

(2) INFORMATION FOR SEQ ID NO: 4065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA 60
 GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA 120
 CGACGCACGC CATATTGACT TGCCATTAAG TCAAAAATTG TAGCAATACG GACTTTGTCA 180
 CCATTGCTA AAGTGACTTG TCGAGTTGGA ATTSGACGAT TGAATATCCC ATCTCCATCA 240
 CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT 300
 GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTTA AGTTCCACTT CTTACCTTCT 360
 TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA 60
 GGAACAATCG TTATTAAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA 120
 CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA 180
 ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA 240
 GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG 300
 NATATTCATT TGTTTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT 360
 GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATT A TTATTAAATT 60
10 ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCTAAAA 120
GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT 180
TTTGCAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG 240
15 AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA 300
ATAAGGGCGG CTGAAGGGGA TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA 360
CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC 400

20

(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAG TGCTGCCAGT TGAGCGCCCA 60
TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT 120
35 TGAGGATAAG ATAACCATTA AGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA 180
AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTAAAGGAAA AAGCTTTATG CTTAAAATAA 240
GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA 300
40 ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT 360
AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA 400

45

(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

AAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300
 GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTcn 356
 10

(2) INFORMATION FOR SEQ ID NO: 4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60
 GCGATTGTCT TTCAAGCATC GTGTTTAAAC GAGTTTGTTG TTAAGGGGCG TTAAAGTAAT 120
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180
 GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240
 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300
 30 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360
 AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

(2) INFORMATION FOR SEQ ID NO: 4071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTCG CTA CTCACAC 60
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120
 45 ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGAACGCCA CATCCTTTTC CACTTAACAT 300
 55

T

361

(2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60
 CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120
 GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180
 TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240
 CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300
 AAACTTGGTA GGAGTATTCT TACTGGATTC CCATTAAACCA TCGTACTTAA TTTTAAATAT 360
 GCGGTTnCCG TnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA 60
 TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120
 GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180
 TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240
 GTAAATGATA CTGAACCAGT TGTGAACCGG AACAAGCAAT GGTAGTTACC AAnATTCTTG 300
 AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360
 CCGGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

| | | |
|----|--------------------------------------------------------------------|-----|
| | TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA | 60 |
| 10 | TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG | 120 |
| | TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC | 180 |
| | CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCCCCAT ATCGGCGGAG TTATGCATCG | 240 |
| 15 | TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAn CTGTATTTCT ACGGACTGAT | 300 |
| | AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTTCAGT | 360 |
| | CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG | 60 |
| | GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG | 120 |
| 35 | CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA | 180 |
| | GCCCCCTCA AGATGAGATT TCCCAACTTC GGTTATAAGA TCCCTCAAAG ATGATGAGGT | 240 |
| | TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA | 300 |
| 40 | AGACTTAATC AAAATAAATG TTTTGCACA AATCCACTTT TACTTACTAT CTAGTTTGAA | 360 |
| | TGATAAATTA CATCCATATG | 380 |

45

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

55

TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120
 CTACTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180
 5 TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300
 AnCGGCATTC TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360
 10 AAGGTTCTTA CCATGGTCAA 380

(2) INFORMATION FOR SEQ ID NO: 4077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATTT AAATCGAAGA AACCAGCAAC 60
 25 AGATTCCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGACCT GCAGCTGGTA 120
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180
 30 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240
 CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360
 35 ACGGGCTCTT 370

(2) INFORMATION FOR SEQ ID NO: 4078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60
 50 TGAATTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

TAAGAGGGGC CAACCATTGT TAGAATAAC AACGGTTGGC TCTTTAATG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

| | | |
|----|--------------------------------------------------------------------|-----|
| 15 | TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA | 60 |
| | TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAAC TTGAT TCTTCTGACG | 120 |
| | CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT | 180 |
| 20 | TTTGACCAAA TGTTGGGATT TTA CTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC | 240 |
| | AGAATGGACC AGGCGCTACA CAGTTCACTC TAATTCCTTT TGGTCCTAAT TCTTCTGAAA | 300 |
| | AAC TTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATAnG | 360 |
| 25 | GCCAGGGAnT AAAACCCTGG ACnAAAGAAG CCGTGGAAT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4080:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT | 60 |
| 40 | AGTAAAATTA AATAAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA | 120 |
| | TATATAGATC AACTTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC | 180 |
| | GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTAAATAT | 240 |
| 45 | GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATTA | 300 |
| | GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC | 360 |
| 50 | AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAATA | 400 |

(2) INFORMATION FOR SEQ ID NO: 4081:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT | 60 |
| 10 | TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT | 120 |
| | CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTTCTGACT CCCAAGTTAA | 180 |
| | ATTAATTGGC ATTCGGAGTT TGTCTGAATT CCGTAACCCG AGAGGGACCC CTCGTACCAA | 240 |
| 15 | ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA | 300 |
| | GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA | 359 |

20

(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

| | | |
|----|--------------------------------------------------------------------|-----|
| 30 | TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTT GTTTTTGAAT TAAATGCATT | 60 |
| | TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG | 120 |
| | TCTTAAAAAC ATTATTTTCCT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG | 180 |
| 35 | AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT | 240 |
| | TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTAAAGATC TGGGGAGAAT | 300 |
| | TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT | 360 |
| 40 | CCAACATTTT nCAGTTTTTT | 379 |

(2) INFORMATION FOR SEQ ID NO: 4083:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

| | | |
|--|-------------------------------------------------------------------|----|
| | TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT | 60 |
|--|-------------------------------------------------------------------|----|

55

TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360
 TGThCnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCCGG 400

10 (2) INFORMATION FOR SEQ ID NO: 4084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120
 25 GTTCTTTCGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT 240
 TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300
 30 TAAATAAACA TTCAAACCTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360
 ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

(2) INFORMATION FOR SEQ ID NO: 4085:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180
 50 GAACCAGCTG GAGCTATAGG CCCATTAAAT TGGAATGAAC AAACATTCAA AACTGGAATA 240
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTGTG TCCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

| | |
|--------------------------------------------------------------------|-----|
| GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAAATTCCA TGTGTAGCGG | 60 |
| TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAACTG | 120 |
| ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT | 180 |
| AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA | 240 |
| AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAAACTC CAAAGGAATT GACGGGCGCA | 300 |
| CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA | 360 |
| C | 361 |

(2) INFORMATION FOR SEQ ID NO: 4087:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

| | |
|-------------------------------------------------------------------|-----|
| GACCTTGCAG GACTCGAACC TGCACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG | 60 |
| AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA | 120 |
| CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT | 180 |
| AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCCTGCAAA | 240 |
| GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC | 300 |
| AGGATTCGAA CCTGCGACCC CTTTCCCAA CCAAGTGCTT TTACCAAGTT GGTACTTCn | 360 |
| GTATAATTTA ACGGGCCCGA TAGGAGTTCG GAACCTTAA | 400 |

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA | 60 |
| 10 | TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTTAA | 120 |
| | GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG | 180 |
| | GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA | 240 |
| 15 | AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA | 300 |
| | AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA | 360 |
| | GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAAATAT | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 4089:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 374 base pairs |
| | (B) TYPE: nucleic acid |
| 25 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG | 60 |
| | GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG | 120 |
| 35 | CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAGTGAG ACAACAACAT | 180 |
| | TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT | 240 |
| | TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA | 300 |
| 40 | TGGATTTAAC ACATTATGAA CGAGATGGTA AACTGCTAG CTCATTGCTG TTGAATTATT | 360 |
| | nCATAACGGT ATCA | 374 |

45

(2) INFORMATION FOR SEQ ID NO: 4090:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 367 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 50 | (D) TOPOLOGY: linear |

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCCGT TGTGACAGTA AGTGACGCGT 180
 5 TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAAT GAACAATGTG ACGTATACGA 240
 CGCAAGACGA ACATGGTCAA GTTGTTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300
 ACAGTGCACC AGTAACAGTG ACACCACanT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360
 10 TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTTCAA 60
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120
 TGGGGTGTGG GCCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180
 GGGTGTGGGC CCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360
 CGGGGGCCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400
 35

(2) INFORMATION FOR SEQ ID NO: 4092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180
 CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

CCGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360
 CATTGACCT TCATTGGTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240
 CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300
 AGCGTATTTT AGTCTCATTG ATTAAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60
 TGTTCCTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTAA AACTCTTTAT 120
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA GCAGGCGCTC 240
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120
 AAGTGAAGGA TGTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA 180
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300
 TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360
 15 CTCCTTGAGA GGAAATACTn ATTT 384

(2) INFORMATION FOR SEQ ID NO: 4096:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60
 30 TTACGCCTTT CGTGCGGGTC GGAAGTTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCGTAG CTTCGCAGAA AGAGCCGACT 180
 CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240
 35 CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300
 GTTAACCCTn AAAGAGCACC CCTTCTCCCG AAATnACGG GGTCATTTTG GCCGAGTTCC 360
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

(2) INFORMATION FOR SEQ ID NO: 4097:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

55

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180
 AGCGATTCGG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC 240
 5 AGCGATTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300
 TCAGATTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTCCGAC 360
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTCAG 400

10 (2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60
 CTGGATTTGA TGTAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240
 TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300
 30 TATTTGTATA TGAATTGTAA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGnAAT 360
 GGCCAGTTTG CCAAGCACTG GTTTGACCA n ATGGnGGCAn 400

35 (2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

45 ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG 120
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT 240
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCCG 300

(2) INFORMATION FOR SEQ ID NO: 4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TAGAACTTGT | TGCCAAACAG | CATGCTTAAT | TTCAATATCT | TCTTTGACTG | CTTCGATATA | 60 |
| TAAATCAGCA | TCATCATTTA | CCAAGTCATC | ATCAAAATTA | CCATATGTTA | AATGACTCGC | 120 |
| TAGATTTAAG | TCGAATAGTA | GCGGCCGTTT | CTTATCTGTA | ATTTTATCGT | AAGATTTTTT | 180 |
| CGCAATGAGA | TTTGGATCGT | TTTTGTCCAC | TACAATATCT | AATAGTTTTA | CTTTAAGTCC | 240 |
| AGCATTCACA | AAAAGTGCTG | CCAGTTGGAG | CGCCCATTTG | GCCTGCGCCA | AGAACGGnTA | 300 |
| CTTTATTAAT | TGGTCATAGT | GAnTCCnCCC | ATTTAGTTGA | GGGATAAGAT | AACCATT | 357 |

(2) INFORMATION FOR SEQ ID NO: 4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TAACTCAGGC | TGGGGACATA | AATCAATATT | CTATGCTCTA | CGAATTATAT | TGGCAGTAGT | 60 |
| TGACTGGnCG | AAAATGCGCT | TGTAACAAGC | TTTTTTCAAT | TCTAGTCAGG | GGCCCCAACA | 120 |
| CAGAGAATTT | CGAAAAGAAA | TTCTACAGGC | AATGCGAGTT | GGGGTGAGGG | CCCCAACACA | 180 |
| GAAGCTGACG | AAAAGTCAGC | TTACAATAAT | GTGCAAGTTG | GGGATGGGCC | CCAACAAAGA | 240 |
| GAAATTGGAT | TCCCAATTTT | TACAGACAAT | GCAAGTnGGG | GTGGGACGAC | GnGATAAATT | 300 |
| TTGCGAAAAT | ATCATTTCTG | TCCCACTCCC | ATCAAAAGAA | TGACAT | | 346 |

(2) INFORMATION FOR SEQ ID NO: 4102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60
 GCGATTACACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120
 5 CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300
 10 ATGAAAATGT ACGTGAGGAA ATThTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360
 CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGTTCAGGTT TAGCTGTGTG 60
 ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA 180
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300
 GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360
 35 AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60
 ATTTTTTTAA AGTATTTAAA AGTAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300

ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

5 (2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60

TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120

20 TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180

GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGGAAAGATT TATTCAAAAC 240

CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300

25 CGGTAACACT TCATAAACT GCGGTTTGTh ACCATTACCT AATnGTCAAG GGTACGGCGT 360

TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

40 GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG ThCCGCTAGA GTAGAACGTn 60

TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120

TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180

45 TTGAAACTG AATGACAATA TGTCAACGTT AATTCCAAA AACGTAATA TAAGTTACAA 240

ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTGATGGGA GAGTTTGGAT 300

CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360

50 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCh 400

(2) INFORMATION FOR SEQ ID NO: 4107:

55

(A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120
 TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180
 15 GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

20

(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

30

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180
 AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTGGT 240
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA 300
 40 AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

55

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300
 TTGCCCCTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCC 360
 CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCG CATTGCGAA AGACTGGCAA GGACCACCAC 60
 GTTTGCAAAA CGGAACAAGT TGGTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAAACAGA GGAGTTAAAG CATCAACATC 180
 CAGCTGATTA TAATGTTTGA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTG GCCATAnGAA 360
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

(2) INFORMATION FOR SEQ ID NO: 4111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60
 GTTGCCTATA CAGCTAAAAA ACTTAATTGA AACGCTGTTA TCTTTATGCC AGTCACTACA 120
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180
 50 ACTGGTGATA CATTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GGCGGTTTAA TTTCCAGTAT TAGTACTAAC

400

(2) INFORMATION FOR SEQ ID NO: 4112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTCACC ATTTTATAA GTCAAACGCT CACATACGGC 60
 TTCGTTTICA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATGTGC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT 240
 TATTCACITCG GntTTGCTTG GGAAAATCTA TATTTTACht ACTTATCTAG TnTTCAATGT 300
 ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360
 GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TCGGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120
 AAGCTGTAGG TGACATTGAA GATTTTTCATC GATGGTCGGT GCCACAAACA 180
 ATCATACGCC GATTGAAGAA AATGTCACITG TTTACCAAGA GATCGTATCC ATTTTATCA 240
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG 300
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360
 TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG | 60 |
| 10 | GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCCC TGGAGTTGGG TCTTTCGGAT | 120 |
| | TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC | 180 |
| | AACCGAAAAT ACTGTAGTCT CTATTTGTTA CAGGATCAAC ATTTTCTTGA ATAACCTGAG | 240 |
| 15 | TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG | 300 |
| | TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG | 360 |
| | nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn | 394 |

20

(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GGCGATTATA TTAAAAGCC AATTACAGAA TGTAGTGGTA ATGAAATATG CCAAGAATGG | 60 |
| | CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT | 120 |
| 35 | ACGATTCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC | 180 |
| | AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA | 240 |
| | AACAGAGCGA GACACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGAAGCTGT | 300 |
| 40 | TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC | 360 |
| | TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG | 400 |

45

(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

55

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60
 25 TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TGCGCCCCGG 180
 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GCGGGGGCCC 240
 30 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGGGCCC 360
 35 CCACCACAGG GAATTTCGAA AGAAATnCT 389

(2) INFORMATION FOR SEQ ID NO: 4118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120
 GACGCTAAGG AGCTTAACTT CTGTGTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA 180
 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT 240

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360
TATnAACCGA A 371

(2) INFORMATION FOR SEQ ID NO: 4119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60
TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120
AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180
TGAAGCTACA CTGCTATTTT CAGCCCATTn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300
ACCATTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60
GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTGCGCG GTAACCTGCA TCTTCACAGG 180
TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CTTTTCGTGC 240
GGGTCGGAAC TTACCCGACA AGGAATTTTCG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360
CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

| | | |
|----|--------------------------------------------------------------------|-----|
| | AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT | 60 |
| 10 | CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATAcataAT | 120 |
| | AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC | 180 |
| | ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC | 240 |
| 15 | ATTGggccAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTc CGCCACCAAA | 300 |
| | CCCTAACATT ACCAGGCCAT ACCAGCAtAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA | 360 |
| | GCGGTGGTAC TACCAAngAC CAGTGGAAGG TnCCAATTAA | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT | 60 |
| | AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn | 120 |
| 35 | ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA | 180 |
| | TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA | 240 |
| | CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT | 300 |
| 40 | ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT | 360 |
| | TT | 362 |

45

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

55

CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120
TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTGAT TTAAGAGGCA 180
5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240
GCGATTCCAA ACATTAATGA nAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG 300
ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352
10

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTGA AGTTCAGGTA AACTGAATG GAGGACCGAA 60
CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120
25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180
TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCCTCTTC GGGTTTACCA ATTTTCAGACA 240
AACTTCCGAA TGCCAATTAA TTTGAACTTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300
30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360
GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAATT TATAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60
ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTTCAA 120
TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180
50 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240
GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTAA GTCAAGCGCT | 60 |
| | CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAAACT | 120 |
| | GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA | 180 |
| 20 | GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA | 240 |
| | TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT | 300 |
| | TACAAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGTnATTC | 360 |
| 25 | AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCGGAT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG | 60 |
| 40 | GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA | 120 |
| | CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC | 180 |
| | GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG | 240 |
| 45 | CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT | 300 |
| | CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA | 360 |
| 50 | TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC | 400 |

(2) INFORMATION FOR SEQ ID NO: 4128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC | 60 |
| 10 | AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTCG | 120 |
| | AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA | 180 |
| | AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT | 240 |
| 15 | GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA | 300 |
| | TCCATTANGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA | 360 |
| | AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC | 400 |

20

(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG | 60 |
| | ATTGGAAGTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC | 120 |
| 35 | CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC | 180 |
| | GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAATAAT | 240 |
| | GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT | 300 |
| 40 | TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG | 360 |
| | TTnAACAGCC GGAT | 374 |

45

(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

ATTAAATTTC AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180
 5 TATATAGTAA TCCGCCTTTT GTTGATACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240
 TCGTAGTATT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300
 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360
 10 TGGATAAAT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTCATCATG 420
 TTGGCGGTTT T 431

(2) INFORMATION FOR SEQ ID NO: 4131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GCGGTTGTTG TCGCATTGTC TGTTTGTTGC GGTGCTTCTA CTTTAGTTGA 60
 GGGCGGTTGTT GTCGCGTTTG GTTTTGATTG CCGTGCTTCT ATTTTAGTTG AGGGCGGTTG 120
 TGATGTGGTG CTTCCACTTT AGGnAAATGA GTGTTGTCGC GTTTGCTGCT TCGGTTGTCG 180
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTG TTCGATACAT TCATTGAATC 300
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360
 35 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCACTG TATGTCTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120
 TGATCATTAT CAGATTCATC TTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180

TCAGCATTAT TTTTATTGT ATTTCGCGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360
 5 ATGGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTGTACC 60
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AACATTGAC TATGGAAGT 120
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAAC GATTAATAGT 180
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240
 25 TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCCG 360
 TAnCGGGTAC CGTTCCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTA CTACGTT 60
 CTACAATTTT ATCTTTTTTTC GTTTTGT CAT AACATCTAA CATGTCGATG GCTTTATCAA 120
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180
 CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTTCG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGC TTCCACGATA | 60 |
| | CAGTCATTTA TTTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA | 120 |
| | ATTTTCAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA | 180 |
| 15 | ATGACATCCG CTTACAGTAT TAAACGCTCA GCCTTTTTTCG TCAAATAATT CGGATTACCT | 240 |
| | GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC | 300 |
| | CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT | 360 |
| 20 | GnATTAAACA ATTTTTGATC GTGGGGGGGC AAATACATAT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4136:

| | |
|----|-------------------------------|
| 25 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 348 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

| | | |
|----|--------------------------------------------------------------------|-----|
| | ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG | 60 |
| 35 | TGGGTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC | 120 |
| | ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC | 180 |
| 40 | TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT | 240 |
| | ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT | 300 |
| | TTATCnTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG | 348 |

45 (2) INFORMATION FOR SEQ ID NO: 4137:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 362 base pairs |
| | (B) TYPE: nucleic acid |
| 50 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTTCTCA 120
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT CACACCACGA 240
 GAGTTTGTA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGGCTGGG 360
 10 AT 362

(2) INFORMATION FOR SEQ ID NO: 4138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180
 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT ACATAAGTAA 240
 30 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300
 TTAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC CAGCGATTAn TTCnTGAGGA 360
 35 ATTCAAGCCT AnTTAAAACC CTTA 384

(2) INFORMATION FOR SEQ ID NO: 4139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC 360
 TTAAAAATAA ATTTAATATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC 240
 CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300
 AAGCCTGTCTG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCgGAAGA GCCTTCCTCT 360
 GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA 60
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA 180
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360
 TnCAAGCnTA TTAAAACTC TTAATCACnC GGTTTTGCnT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC | 60 |
| | TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA | 120 |
| | CTTGCCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC | 180 |
| 15 | CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT | 240 |
| | TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC | 300 |
| | GCCAAGCCAT TTTCCTTGGG TTACTIONTAA TTGACGTTT AAGGCATAAA AAAAAGAGAC | 360 |
| 20 | TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCn | 400 |

(2) INFORMATION FOR SEQ ID NO: 4143:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TTTAAAATTG ACATTATTAC TGACCAAACA AGTGACATG ATCCGCTAAA TGGATATGTG | 60 |
| 35 | CCACAAGGAA GCGAAAGTAT TCGTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA | 120 |
| | AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CCAAAAACGT GCGCTGTAG | 180 |
| | CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT | 240 |
| 40 | TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG | 300 |
| | GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG | 360 |
| 45 | GAGGAAATG | 369 |

(2) INFORMATION FOR SEQ ID NO: 4144:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60
 ATGTTTTAGT TGCAC TAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCCTCGAC ATAGTGCCAC 180
 ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTCCCCCTGT CTTCTAAATC 240
 AACTAATTTA AGCTGTGCT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAAACAA 360
 CGGGAGnGGC 370

(2) INFORMATION FOR SEQ ID NO: 4145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCAGAAATAT GTACCTAAAT TACAGTCACA TGAAGTCCGT 60
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCGGACG TTGCTGGAGG TCTTGAAACA 120
 GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180
 30 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240
 TTGCTTTGTA GTCAGACCAG AACAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300
 ATCGCACTTC GGCATTGTTC CTAACGCCCT AATTnAATT AAnTAATGTT CAAAGTAGGA 360
 35 TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTTT TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGTTGTC 60
 50 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTTGATCA TACTAAATTT 180

GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTTnTTTT ATCAGGAGGA 300
 GGATGGCGGT ATCCAATTTA TTTCCATTG GAAATATATG GnCCCCCGTT TTGGGAACnC 360
 5 ATTTTTTGGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA 120
 CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCAATCATT TGTCCCACCT 240
 25 TCGACGGCTA GCTCCTAAAA GGTTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTGn CTGGGTTTAC 360
 nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTTGAA AATGATGAAC GATTCAGTGG 60
 TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATCCGTGG 180
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240
 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300
 50 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGCnCTA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA | 60 |
| | CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC | 120 |
| | AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT | 180 |
| 15 | TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGGTA TTGTAAGTGG | 240 |
| | CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TAACTGAAG TAATCTGATT | 300 |
| 20 | GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA | 360 |
| | AACCATCATC ATATTnCnCAT CTGGTTAGGA CTGAAATGGC | 400 |

(2) INFORMATION FOR SEQ ID NO: 4150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT | 60 |
| | CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG | 120 |
| | GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT | 180 |
| 40 | ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG | 240 |
| | TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG | 300 |
| | GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG | 360 |
| 45 | AATAGGCGTT A | 371 |

(2) INFORMATION FOR SEQ ID NO: 4151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnTAATT TTCCTTATAT 60
 5 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180
 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240
 10 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360
 15 TCGTTT 366

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360
 TCGCnTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

(2) INFORMATION FOR SEQ ID NO: 4153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

(2) INFORMATION FOR SEQ ID NO: 4154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60
 nCAGATTGTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120
 CATACTCCA TCTCACC AAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360
 30 CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60
 45 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCG AGAAAGAACG TAAATTTAAT 180
 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240
 50 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300
 AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

(2) INFORMATION FOR SEQ ID NO: 4156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA 120
 CTGCCGGTGA CAAACCGGG GAAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240
 CAAATCCCAT AAAGTTGTTT TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300
 GGAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGATTACGT TTCCCGGGGT 360
 CCTTGTTACA CACCGCCCGT 380

(2) INFORMATION FOR SEQ ID NO: 4157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACTTA 60
 TGGATGATGG ATTCTGCCAA GTTAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTC TAAAGGGCAA 240
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TCGTCAGGA 300
 GTTTCAGTGG ACCAGCTGGG GTGGATTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360
 ACTTAACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

15 (2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60
 TCTCTTGtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240
 GGAACCTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCGTCTCG ATGACCTGGT 300
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTTCTTCT 360
 TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCGT 420

40 (2) INFORMATION FOR SEQ ID NO: 4160:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

55

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300
5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60
20 GGCCGGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120
TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180
CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240
25 AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA GAAAAGCCTC TAGATAGAAA 300
ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTAT 60
TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120
GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180
45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240
GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300
GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360
50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 4163:

(A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT | 60 |
| | AAAATAATAC CAATCTCATT TTTAAATTCT AAACCTGGTT TCGTATAATA CGCTCTTAAA | 120 |
| | TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG | 180 |
| 15 | TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTTG ATGGAGGTGT TGTCACTTTA | 240 |
| | GTTGnAAGGC GGTGTTGTCT CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG | 300 |
| 20 | CGGTGTTGTC GCGTTTGTTT TTGnATGCGG TGCTTCTATT TT | 342 |

(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

| | | |
|----|--------------------------------------------------------------------|-----|
| 30 | TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC | 60 |
| | TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCCTTCGC GTTGCTTCGA | 120 |
| 35 | ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTTC AACCT | 180 |
| | TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA | 240 |
| 40 | AACCCCTTAA AACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC | 300 |
| | CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGGCCA | 360 |
| | nGGGGGTnCC nCCAAAACCTT TGGGGATTTA ACGGTAAAAA | 400 |

(2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

55

GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120
 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180
 5 ACTGTCTCAC GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240
 TATTCACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTACTAATnG GTTGCCGAAT 360
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 240
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAATAAT CCnGGTnGTC 360
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60
 50 AGATACACAC CTTTACCGAC TATTTAAAAT AACTTCACC AATTCATTTT AATTTAATGG 120
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180
 ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTTTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT 358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA 60
 TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTTCT AAATATGCAT 120
 ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT 180
 GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT 240
 CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA 300
 TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAntTG AGAGCTTnTG GnTTAGCTGG 360
 ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT 400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT 60
 TCGTTAAATA AACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA 120
 ATTCAGGTCT CTTCCACGTC ATATTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG 180
 AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TTGTTTTTCC 240
 GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACTTCA ATGTTATCAA 300
 TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC 360
 GTGTACnTCC ACGGTTTTCA TTTAAAnAACA ATTTACCGGA 400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA | 60 |
| 10 | TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGGGC ACTGTCTCAA | 120 |
| | CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA | 180 |
| | AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA | 240 |
| 15 | TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGrAGGCGCT GGGTGGGGAT | 300 |
| | ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT | 360 |
| | GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG | 395 |

20

(2) INFORMATION FOR SEQ ID NO: 4171:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 371 base pairs |
| | (B) TYPE: nucleic acid |
| 25 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG | 60 |
| | GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA | 120 |
| 35 | GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC | 180 |
| | TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT | 240 |
| | CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA | 300 |
| 40 | CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT | 360 |
| | CGAAGTGGCG C | 371 |

45

(2) INFORMATION FOR SEQ ID NO: 4172:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 361 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 50 | (D) TOPOLOGY: linear |

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAAACGCG 180
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CChGAATGAA CCGGTACGTG 300
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCCG GACTATAAAA 360
 10 T 361

(2) INFORMATION FOR SEQ ID NO: 4173:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360
 AGnAATCCCA CCGTTGTAnG 380

35

(2) INFORMATION FOR SEQ ID NO: 4174:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTGGAAGTC GTTGATTTCa CACTGCCGAG 120
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG 180
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

55

GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 4175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGAAGTGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120
 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAAGTTCTG TGTTCGGCAT GGGAACAGGT 180
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240
 AGTAAGTAAA AGTGATTTTG CTTGCAAAA CATTTATTTT GGATTAAGTC TTCGATCGAT 300
 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60
 GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTTGGTA CTTGTTTTGT GGTGCGCAT 120
 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTTGTGGCG TGTGTTTGA TCGAGGTGTT 180
 GTCACTTTAG TTGAAGGCGG TGTGTCGCA TTTGCTGTTT GTTGCGGTGC TTCTACTTTA 240
 GTTGAGGGCG GTGTTGTCGC GTTGGTTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG nAATGAATCG CGATGGAATA TCTCTATCTG nAAACAGATT TCTTTTGTGTC 60
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTGCG CTTCTTTATC AATGTCATAA 120
 CCTAATGCTT TTAACCTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA 240
 ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGA nATTAAA TCCGAGGTTT TAGTTCCTCG 360
 15 AG 362

(2) INFORMATION FOR SEQ ID NO: 4178:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTGAACCG CATGGTAAAG nTGGAAGAC GGTCTTGCTG 60
 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120
 30 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGA CACGGTCCAG 180
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC 240
 35 GCCGCGTGAG TGATGAAGGT CTTCCGATCG TAAACTCTG TTATTAGGGG AGGACATATG 300
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTACTAGGGG 360
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

(2) INFORMATION FOR SEQ ID NO: 4179:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

50 GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

55

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180
CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTTCTGTCG TCTAGTTGGA 240
5 AGAGAACGGC GGTGGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360
10 GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60
GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120
25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180
TAGTAACGTC CTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT 240
30 AATCTATGTT TCCACCATTT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300
nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60
45 TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA 120
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180
50 TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTCTGATC CCGCTAGTCT CCACCATTAT 300
TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120
 GTCGATCTGC TAATTTTGCA AGTGTCAC TG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180
 CTTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATT C CTCTTCATA 300
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTTCA 360
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

(2) INFORMATION FOR SEQ ID NO: 4183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTA 60
 ACACAGCTGC AGGTGGTTCA TGGATTTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT 120
 ATTCACTTCA TGCGGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGTC CGACATGTTG nATGCTGGCT 240
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TGCGATAGGT AATGGTTTAG TCGCAACACC 120
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT 180
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GACTAAGTA CTACAGTTTT 240
 10 CAGTATGTTA CAACTAAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300
 CATTGTATTG ATGnTCCTTG GGTnCATTTG CTGCATACAT GA 342

15 (2) INFORMATION FOR SEQ ID NO: 4185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

25 AAGCATACTC TGAAGCGGTG AACAAAATA GAACAGATCA CATTAGACAT TTAATTGAAT 60
 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTCAGC GGAACACATG AAACGTTAGC 180
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240
 CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

(2) INFORMATION FOR SEQ ID NO: 4186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTG CATGAACCCC AAGCGTTTGC CGCATGATGC 120
 TGTTTATTTA ATTTATGGAA TGTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

55

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360
 GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

5 (2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACChCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120
 20 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180
 TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240
 AGAGCCCGTT AATGGGTGAT GCGGTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTTG 300
 25 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60
 40 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGGAA AGGTGAAAAG 120
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180
 GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240
 45 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300
 TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

50 (2) INFORMATION FOR SEQ ID NO: 4189:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTTCAACAAC 120
 TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACTTCCCC 300
 AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCCTCT 358

15 (2) INFORMATION FOR SEQ ID NO: 4190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60
 AAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180
 ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300
 35 AAACCTAAAT ACGGTGGTAA TACCATTGT GTnTATTTGTT GTGAAGTATT GCGGTCATAA 360
 TA 362

40 (2) INFORMATION FOR SEQ ID NO: 4191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

50 TGATCACCCA TGTCTGGAC TCCCAATTGA AATTGAATTG GGCATTCGGA GTTGTCTGG 60
 nATTTCGGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

55

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240
 CATTCAGTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300
 5 ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA 360
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT 120
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180
 25 TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300
 GTTGTCATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360
 30 CCAATCGGAA ATTGTAGCAT CnTTAATTTC CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60
 TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATThTCATA TAATCCGGnA 360

(2) INFORMATION FOR SEQ ID NO: 4194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300
 AGTTtACGAT TTGgATtGCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

(2) INFORMATION FOR SEQ ID NO: 4195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG GCAACGTTCT 60
 ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACCTT CTGTGTTTCGG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

(2) INFORMATION FOR SEQ ID NO: 4196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120
 5 GAAGCAGGTG CGACACGTAT TGGTCCGAGC GCnGTGTTCA AATTATGCAA GGTTTAGAAG 180
 CAGATTCAGA TTACTAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240
 ATCGTGTACA TTTAATCGTA ATGGATTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300
 10 ATTTTAAAG ATGGAGGTTT ACATACTTTT A 331

(2) INFORMATION FOR SEQ ID NO: 4197:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTCT GCATGGGTGC 60
 25 AGCTGCTATA TTTGAATATG TCGGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120
 TGTTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180
 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240
 30 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATAn TATTGCTAAT GCnAGTAACT 360
 35 nATCTGATTG T 371

(2) INFORMATION FOR SEQ ID NO: 4198:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGThATTc TACCGCTGAA CTACTTCTGC ATATGCGGGT 60
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

55

TAAGAATAAA TGGTGGAGAA TGACGGGTTC G_nACCGTCGA CCCTGTGCTT GTTAAGGCAG 360
 ATGCTTTTCC CACTGGGGTA AATTTTCCGA TTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120
 CCATCCTAGT ACGCCAATAC CATTTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCAGGAACA TGTACAACAC TTGCTAAATA 240
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300
 ATGCTTTCGG TTGGCCCAAT TTAAAAAACT GGATAACGTT CAT_nGTTACG TTCCAATTCC 360
 TAATTTCC_nA ATTACGGTTC CA_nGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60
 CGTGCTACTA _nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240
 CACACCATGG TTCAATGC_nT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTG_nC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT | 60 |
| 10 | CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC | 120 |
| | AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC | 180 |
| | AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG | 240 |
| 15 | TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG | 300 |
| | TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA | 360 |
| | GCGGTTGGAC | 370 |

20

(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGTnGG AATGAGtCGG | 60 |
| | gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC | 120 |
| 35 | CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT | 180 |
| | GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTTGT GTTGGCTCGC CGCCTGAATT | 240 |
| | CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTG GTCTAGTTGC | 300 |
| 40 | TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTC | 360 |
| | AAAGCAGCGT GCAAAAGGTT | 380 |

45

(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

55

GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTTGTAGAT 120
 CCAGGTCCAA CTGGTTTAGA AAAGAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT 180
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360
 10 CCGTAATCCA GGTACCACC CTCCnnGGnT GGATTTAGGA 400

(2) INFORMATION FOR SEQ ID NO: 4204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

(2) INFORMATION FOR SEQ ID NO: 4205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAACAACA AACTTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60
 45 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT 120
 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180
 50 GTTGAAATAC TCCCGCATT TATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

(2) INFORMATION FOR SEQ ID NO: 4206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACATAA GTGTGAATAT TACATTCCCA 60
 AATCCAAATC AATATAAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60
 CAAAACCTGC TTAAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTttCAATC GGTGAATGCA ATGwCATAGG 180
 GCTTGGTCCA TACACCTTTC CAAAATTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360
 AATGTAACAC GCCGGTGA CT CATCCAGCT GAATAGACGC GT 402

(2) INFORMATION FOR SEQ ID NO: 4208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360
 15 CAGCATCTGG TACnGGTAAG 380

(2) INFORMATION FOR SEQ ID NO: 4209:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

25 AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360
 ATTGGCCCCG TGCCAACnTT TATATTGAAC CAAGCACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4210:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCACAACC ACAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

55

AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAAG TTTCTTCTAA ACAGACTTCA 180
AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240
5 TGTTAGGCCGA TGCAGAGTGC GATTAGGCAG CTACTGCGAA ATTATTGTnT GATTTGCCAG 300
TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

20 AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC 60
GTTTTCACTT CGCCAAGCCA TCITTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120
AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180
25 TTCTACTCTA GCGGAACGTA AGTTGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240
TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300
ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

30 (2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

40 GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
45 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240
TTTTAGCACA TAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300
50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

(A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAA TCGTTACGCC TTTCGTGCGG 60
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120
 TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

20

(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

30

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT 60
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTAATCATTT 120
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAAnTG TGGACAACGn 360
 TGG 363

45

(2) INFORMATION FOR SEQ ID NO: 4215:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

55

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTCGAACCG ACACTCCACA 180
 5 AGTGGAACGG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240
 AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300
 CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGACTACC 338
 10

(2) INFORMATION FOR SEQ ID NO: 4216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTTCAGT 120
 25 TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTAA CCAGATCCAG AAAGTGCTTT 300
 30 AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

(2) INFORMATION FOR SEQ ID NO: 4217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 50 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA 300

(2) INFORMATION FOR SEQ ID NO: 4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

| | |
|---------------------------------------------------------------------|-----|
| GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA | 60 |
| AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCCTCA | 120 |
| GTTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT | 180 |
| TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC | 240 |
| TATTCAGACT CGCTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT | 300 |
| AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATT | 345 |

(2) INFORMATION FOR SEQ ID NO: 4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

| | |
|---------------------------------------------------------------------|-----|
| TCTTATGACT GCTTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AAACGTTTTTC | 60 |
| ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA | 120 |
| AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC | 180 |
| TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTCG | 240 |
| GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA | 300 |
| CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACChTTAT TTTGGTTAGT | 360 |
| CTTCGTC | 367 |

(2) INFORMATION FOR SEQ ID NO: 4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60
 5 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180
 nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240
 10 TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300
 CGGCATGGGA ACAGGTGTGA CCCCCnTGGC TATAGTCACC AG 342

(2) INFORMATION FOR SEQ ID NO: 4221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60
 25 TGTGAACTCT TGGGGGAGAT AAGCtGTTAT CCCCggGGTA GCTTTTATCC gTTGAGCGAT 120
 GGCCCTTCCA TGCgGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180
 30 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT 240
 GAGGGAACTT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACCTGC 300
 35 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

(2) INFORMATION FOR SEQ ID NO: 4222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60
 50 TTACCAAGCA AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA 120
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360
G 361

5 (2) INFORMATION FOR SEQ ID NO: 4223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60
TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120
20 ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180
ATAGAGCGTT TGA CTACGGA TCAAGAGGTT ATGGGTTCGA CTCCTATCGG GCGCGCCATT 240
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300
25 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

40 CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60
GAGTGA CTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180
45 TAGTGTCA TT TCCAGCAATT TGTTCGGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300
CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360
50 TTCGATCCAG TTGGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

55

- (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

10 GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTACCA TTCAACCAA ATTGATCCTG 120
 TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180
 15 TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

20

(2) INFORMATION FOR SEQ ID NO: 4226:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

30

TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60
 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAnGTAAG TTCGnACTAC 120
 35 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300
 40 TCCACATGTC ACCATGCTTC CACCT 325

(2) INFORMATION FOR SEQ ID NO: 4227:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TTnTTCAACA 60

55

AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAACTCCTA TATTAGTTGG 240
 5 AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

20 AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60
 TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120
 GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180
 25 AACTATGCCC CTATTAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

(2) INFORMATION FOR SEQ ID NO: 4229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

40 CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAATTTAG AGGTGATGTT 240
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC 360
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCTTC 60
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TATCGGTCAC AGAGAGTATT 120
 TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTACTCA 180
 GGATCCACTC AAGAGAGACA ACATTTTTCGA CTACAGGATT ATTACCTTCT TTGATTCATC 240
 TTTCCAGATG ATTCGTCTAA TGTCGTCTCT TGTAACCTCC TATAGAGTGT CCTASAACCC 300
 CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG 339

(2) INFORMATION FOR SEQ ID NO: 4231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAGTCATAT GCATACACTT GGTTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG 60
 AATTTCGTTA CCTGCGCCTT CTTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120
 TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC 180
 AAACTTTTTC ACTTCAGACT GACGTCCGTh TTTAGTTAAT GGGTCAATAA TTCCATAACG 240
 ATGAGTATCT GCTTCCGGAA CTTCTTGGAC ACCTATAACT GAGTGCCCTG ThTCTTCATA 300
 AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

(2) INFORMATION FOR SEQ ID NO: 4232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTATATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG 180
 5 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAkTCA 240
 AGCTCCCTTA TGcCTTTTACA CTCTATGAAT GATTTC AAC CATTCTGAGG GAACTTTGaG 300
 10 CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG AACTGTCTC 360
 CCACCACGAT AAGGTCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180
 AATATATGTT AAGTGGAAAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240
 30 AAGCAGCCGT CATTTAAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

(2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60
 45 ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180
 50 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTATGG AGGGGTAACG AnTGGGCTAA 300

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

400

(2) INFORMATION FOR SEQ ID NO: 4235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA | 60 |
| | GGCGTAATAT CACTCTTTGC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA | 120 |
| | TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT | 180 |
| 20 | TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCTAAAC CACTATCTGA TACAAGACCA | 240 |
| | ATTGCATGnT TTGTTGGGAA AATCATTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA | 300 |
| | CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T | 341 |

(2) INFORMATION FOR SEQ ID NO: 4236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCTTAAAT ATAATTTTAC | 60 |
| | AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCCGA CCTCACGGGT ATGAACCGTA | 120 |
| 40 | CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA | 180 |
| | GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCAG CTGAGCTAAG | 240 |
| | CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC | 300 |
| 45 | CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT | 360 |
| | TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA | 400 |

(2) INFORMATION FOR SEQ ID NO: 4237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5 nAntTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60
 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180
 10 ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAG GTGCTTTGAC AATGACCGTA 240
 CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300
 CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTTCGTATA AACATTAAATT 360
 15 GTATTTTCAG GAAGTC 376

(2) INFORMATION FOR SEQ ID NO: 4238:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

25 CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120
 30 TTTTCTGGGA AAAGTTTGCG CATTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240
 GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTCACTCCG TATTGAAGGC TACTTGACGA 300
 35 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

(2) INFORMATION FOR SEQ ID NO: 4239:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

45 CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60
 50 TTCGGACACG TAGAAAGATT TATTCAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

55

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240
 AATGCAAAGG CGCCATCAGG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT 300
 5 GAACTACATT ACATTTGTCC AATACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60
 20 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120
 TTATGAATGG CATACTGCT GTTGTTTATG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180
 CAAGTGCGCA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240
 25 TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

30 (2) INFORMATION FOR SEQ ID NO: 4241:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120
 45 CTTTATGTTG GGGCCCCGCC AACTTGCAAT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180
 TGTGTTGGGCC CCGCCAACCTT GCATTGTTTG TAGAATTTCT TTTCGAAATT CTTTATGTTG 240
 GGGCCCCGCC AACTAATTC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300
 50 GGACTTTTAT GCGGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

55

(A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA | 60 |
| | TCATCTAAAT GATTTTTAGC TGTGATTAAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC | 120 |
| | TCTTGTACTT CTTCAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG | 180 |
| 15 | CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA | 240 |
| | TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTTGAACC ATAATCTTTC | 300 |
| | ACAATTnCAG TTGTGTTGAC AGATGAGnGG CCGTGcAGTA AGGACTGGAT ACACTACGAG | 360 |
| 20 | TGACCGGACT GCTTCGGGnA ATGTGATGA | 389 |

(2) INFORMATION FOR SEQ ID NO: 4243:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT | 60 |
| | TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT | 120 |
| | GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT | 180 |
| 40 | GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTh TTTTGGAAT GATTGCGGCG | 240 |
| | ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT | 300 |
| | AAACGACAAG GTGCAATTTT GG | 322 |

45 (2) INFORMATION FOR SEQ ID NO: 4244:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120
 ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180
 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240
 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT 300
 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

(2) INFORMATION FOR SEQ ID NO: 4245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCTATTT CACTCCCCTT 60
 CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120
 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTAATC 180
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTC 240
 ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAATC CCGTATAGAG TGTCCTACAA 300
 CCCCACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGnAA 358

(2) INFORMATION FOR SEQ ID NO: 4246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTTCGG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CCGATCACTA 60
 AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT 120
 ACACTCTATG AATGATTTCC AACCATCTG AGGGAACCTT GAGCGCCTCC GTTACCTTTT 180
 AGGAGGCGAC CGCCAGTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG 240
 GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC 300
 TCACGTTTCA AAGnTCTACC TATCCTGTAC A 331

(2) INFORMATION FOR SEQ ID NO: 4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG 60
 ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG 120
 GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTCT TCATTCTTCA AATAAACCAG 180
 AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG 240
 GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA 300
 ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC 360
 TAATGCCCAA T 371

(2) INFORMATION FOR SEQ ID NO: 4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60
 ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120
 5 TGTGCGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180
 TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240
 10 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300
 GTTTCATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

(2) INFORMATION FOR SEQ ID NO: 4250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

GAGCCCAAAC CAACAAGCTT GCTTGTTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60
 25 AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180
 30 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GCGGTGCCTT TT 352

(2) INFORMATION FOR SEQ ID NO: 4251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

CATTTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTCAC 120
 50 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240
 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

(2) INFORMATION FOR SEQ ID NO: 4252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

| | | |
|-------------------------------------------------------------------|-----|------|
| TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT | 60 | 1 |
| AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC | 120 | 15 F |
| TTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC | 180 | C |
| ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT | 240 | F |
| ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT | 300 | 20 F |
| TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTAAAT | 360 | 1 |
| TCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC | 400 | 25 C |

(2) INFORMATION FOR SEQ ID NO: 4253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

| | | |
|-------------------------------------------------------------------|-----|------|
| AAGGTATCA AAGATGTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA | 60 | F |
| CTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA | 120 | 40 F |
| TTATTTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA | 180 | C |
| AAAGATGCA GATGGTGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT | 240 | 1 |
| ATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGA CTC | 300 | 45 C |
| GnCAGCGAC TCAGACTTCA GACAGCG | 327 | F |

(2) INFORMATION FOR SEQ ID NO: 4254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120
 TAGGATTGTh CTnTTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240
 GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

15 (2) INFORMATION FOR SEQ ID NO: 4255:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60
 CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTC 120
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTAAATACA 180
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA TATAATTCAA AAAAGGGTCG 300
 35 AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA 344

(2) INFORMATION FOR SEQ ID NO: 4256:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTTCAAT ATTAAATTGC 60
 50 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120
 AAGCTAAATT CTGCGACAAA GCCGCCCAT TGCAGCACCGA CAGCCACACC AATATTTTGC 180
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTTG GCCCACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

(2) INFORMATION FOR SEQ ID NO: 4257:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

15

GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCC GACTAT TTTTGAAAAG AGCGTGTTAC 60

ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120

20

TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180

AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240

TTCGGTTTTG AGACAATTCG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300

25

TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360

GCGGAGTGA 369

(2) INFORMATION FOR SEQ ID NO: 4258:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

40

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

TTTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC 120

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180

45

GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240

ATGTACCAGT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA 300

CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT 335

50

(2) INFORMATION FOR SEQ ID NO: 4259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTGTA 60
 GCTTCGCAGC ACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180
 10 CTGCGGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300
 CTGTGTCGGT TTGCGGTACG GGCA 324

15 (2) INFORMATION FOR SEQ ID NO: 4260:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG 60
 CATTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAGAA ATTGTACATT 120
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 180
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAntT 300
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

40 (2) INFORMATION FOR SEQ ID NO: 4261:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

55

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240
 TTGTCTTGTT TATATTATGT GATTCAAACA TTAGTAGTCT TGGTAAATCT AATTCGTAAA 300
 5 ATGCTAAATC TAACCATCTA TTAAATTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60
 20 ATTTTGACGT TTAGGCATA AAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTGACTTGT GACAATCGCT TGChTCTTTC CTCTCCTTCG GCTCTCGCTT 240
 25 ACTCATtnAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCTAC GnaATGTCGG AACCACAATC 60
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA AATAATAAAT 180
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC | 60 |
| 10 | AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA | 120 |
| | TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTGCTGT | 180 |
| | TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA | 240 |
| 15 | ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC | 300 |
| | TTTTTGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T | 351 |

20

(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

| | | |
|----|-------------------------------------------------------------------|-----|
| 30 | ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT | 60 |
| | GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA | 120 |
| | AGTAACGCAA TCATTTCTTC TAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA | 180 |
| 35 | TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC | 240 |
| | ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA | 300 |
| 40 | CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT | 346 |

40

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG | 60 |
| 55 | GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC | 120 |

55

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240
 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TCGTCTGCC AATTCCGCCA 300
 5 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTTT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60
 20 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTTCGCA GTGTTTGCTG GTTGCGTGAG 120
 GTnTGTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180
 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240
 25 ATTA AAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180
 TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240
 GAATCGTTCA TCATTTTTCa nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120
 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

20

(2) INFORMATION FOR SEQ ID NO: 4270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30

AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTTGTCCATT 60
 TTATTTTTTA ACCAAAATTT GATTAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120
 35 TAAGTCGACT ACCATCGACC CTAAGGAGCT TAACCTCTGT GTTCGGCATG GGAACAGGTG 180
 TGACCTCCTtT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAC TAGATA 240
 GTAAGTAAAA GTGGATTTTG CTTGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300
 40 GTATTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360
 CGCAGGGAnC 370

45

(2) INFORMATION FOR SEQ ID NO: 4271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

55

ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTAA CACAATTATG ATTGGCGTAA 120
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTCTGGT CCGGCACTTG TGGCACAATG 180
 5 GaTTAATTAA CAATATTATG CGTCGACAGT TCGCCGCAT TTTTaCGGtA ATGGGAATAA 240
 AGCGACACAA ACCGTCACGT CAGTGTTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300
 GTAGGGCTTA TCATGGCCAA TCTGTAA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAACCTT 120
 25 TCAAACTTAT CGATGATTTC ACCGTTATGA ACTTTCACAG CTGCAAnTCG ATGATTTTAT 180
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACTTCC 300
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTAAAGA TGACTCTAGA CTCTTATGTT 60
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120
 TATAGAATGG TGTCATACCT GAACCATAAT CCTTAACTGG GAAACATCA ACAGTCTTCT 180
 50 TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTTTCAA ATCATTCTTA AGTGTGTCGA 240
 TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA | 60 |
| | GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA | 120 |
| 15 | GTTGCTTCTG GGCCTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA | 180 |
| | ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA | 240 |
| | TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG | 300 |
| 20 | CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG | 360 |
| | GAAAAATGGC GAATTAAGGT TGChGATTTT CCCCGGGTAA | 400 |

(2) INFORMATION FOR SEQ ID NO: 4275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC | 60 |
| | TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT | 120 |
| | TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA | 180 |
| 40 | TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG | 240 |
| | GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT | 300 |
| 45 | TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n | 341 |

(2) INFORMATION FOR SEQ ID NO: 4276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCTT 60
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTT TTTATTTTAA ACATGAACAA 120
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180
 TTAAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240
 CATTCCATTA AACCACCTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360
 ACGGTCCG 368

(2) INFORMATION FOR SEQ ID NO: 4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTA CTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60
 GAGGGACCAA ACATTGGATT GATTAACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120
 30 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180
 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACCTCTAAA 240
 TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

45 CACTTGTACT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60
 50 CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120
 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG 180
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

TACTTATGCT CATTGGATGT TGAATCGGAT TTA CTTTCAC TTGAATGATG TTGAGTCGGA 360
 TTCAC TTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATT TAAAAG ATATTAGACA TAAAATCTAA AAnCAGCAGT AAGATGATTT 60
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120
 20 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTTAC 180
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240
 AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC 300
 25 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
 40 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240
 45 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300
 CCTATAATCG TTTAATCGAT GGGGGG 326

50 (2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG 60
 GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGGAAT ATATCCTTAG AAAGGnAGGT 300
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATT 360
 GTGCCCAAnCn 370

(2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

30 GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60
 CTTACAGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300
 GAAACATTAG GnATATCTCT TGTGATTTC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn 400

(2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

55 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

TCTGTCCCAC TCCCGATTAT CTCGTGCGAA TATTTTTC AAAGCGATT AAATCATTAT 180
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTGGA TTTGGTGAAA 240
 5 TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTAAAT nCCATATTGT GCTCTTATAT 300
 CTnAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAAC TTCTATTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTGTC 180
 25 AAGATGCGTT ATAAGCATTG GCGCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300
 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTACGTG 360
 30 ATGTCTAACA AGTTTTnTn GCTAAAATCn GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTCTT TGTGTTTACT TTTATTTTG ACGTTT TAGA CATAAAAAA GAGACTCACG 60
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180
 TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240
 50 TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTT ATTTTGACGT TTTAGGCATA 300
 AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480
 ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT 540
 5 TTCTTTTG TG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG G_nATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAGA CGGTCTTGCT GTCACCTATA 120
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240
 25 GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGC_nGAAACTG GACGGAGCAA CGCCGCGTGA 300
 TG_nATGGAAG GTCTTCGGAT CGTAA_nACTC TGTTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGT_nACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60
 CATCTTTAAT GACAACTGTA CCATTTTTC_n CAACATTTAA TTCATCTAAT TCCTTACCCT 120
 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180
 45 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300
 50 GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

| | | | | | | | | | | | | | | | |
|----|--------|-------|--------|-------|--------|-------|-------|--------|-------|--------|-------|--------|------|----|-----|
| | CTATTC | ACTG | CGGCT | CTTCT | GGGCG | TTAAC | CCTAA | AAGAG | C | ACCCCT | TCTC | CCGA | AGTT | AC | 60 |
| 10 | GGGGT | CATTT | TGCCG | AGTTC | CTTAA | CGAGA | GTTCG | CTCGC | TCAC | CTTAGA | ATTCT | CATCT | | | 120 |
| | TGACT | ACCTG | TGTCG | GTTTG | CGGTAC | GGGC | ACCTA | TTTTTC | TATCT | AGAGG | CTTTT | CTCGG | | | 180 |
| | CAGTG | TGAAA | TCAAC | GACTC | GAAGA | CACAA | TGTCT | TCTCC | CCAT | CACAGC | TCAG | CCTTAA | | | 240 |
| 15 | CGAGT | ACCGG | ATTTG | CCTAA | TACTC | AGCCT | TACTG | CTTAG | GACGT | GCAAT | CCAAT | CGCAC | | | 300 |
| | GGTTT | nGCCT | ATCCTA | | | | | | | | | | | | 316 |

(2) INFORMATION FOR SEQ ID NO: 4289:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

| | | | | | | | | | | | | | | | |
|----|--------|-------|--------|-------|--------|-------|-------|-------|---------|--------|-------|-------|-----|--|-----|
| 30 | TTnTTT | TATGT | CTAAA | ACGTC | AAAATA | AAAAG | CAAAC | ACAAA | GAAAG | ATGGC | TTGGC | GAAGT | | | 60 |
| | GAAAAC | GnTT | GAATC | TGACG | AAACG | AGAAA | TGTAA | AGTAT | AATAAAA | AGC | AGTC | AATA | AGA | | 120 |
| | TGATT | TCAAT | TAGAA | ATCAA | TTTAT | GACTG | TTTTT | CTTAC | TATGT | GTAA | ATTA | ACA | ATG | | 180 |
| 35 | AATATA | AACAT | CTTAT | TTTCA | TTAAT | ATAAA | TATTG | GAAGG | ATCGA | nATGA | TTTAC | ACGTT | | | 240 |
| | GTTTG | AGTTG | TATTAA | TCA | TCATG | ATCTT | TAAGT | TGAAT | ACCA | ATAATG | ACAGT | ACCTG | | | 300 |
| 40 | TATTTT | GAGA | GATTTT | TTTAA | GT | | | | | | | | | | 322 |

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

| | | | | | | | | | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|--------|-------|-------|--------|-------|--------|--|--|-----|
| 50 | TCATT | TAGCT | CTACT | AAACT | CGTTG | CGCTC | TTTTC | TCGTT | TCGTC | CAGATT | CAAAC | GTTTT | | | 60 |
| | CACTT | CGCCA | AGCCA | TTTTT | CTTTG | TGTTT | ACTTTT | TATT | TTGAC | GTTTT | AGGC | ATAAAA | | | 120 |

55

CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACTCGTTG 300
 5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT 120
 GCTTTTTTCAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180
 TTAAGGCGTT ACTTTACCAA CTAAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGGAATGATC 300
 TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360
 30 TTGCAAGATG GAATGAGAAG TGAACACAGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60
 GGCATAAAAA AAAGAGACCT TCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTTGCCT 120
 45 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240
 50 TACTAACTC GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 300
 GCCATTTTTT TTTGTGTnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTAAAA 60
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTTCGAT 120
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AAAGTGAATG ACAATATGTC 180
 15 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240
 TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

20

(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

30

TTATCACCCA TGTCTGACT CCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120
 35 GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT CCATTCAGTG 240
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300
 40 AAACGCCCTA TTCA 314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

55

GCAATCTATC TGTGAAGAC ATTGATTGA TCGAATTGAA CGAAGCATTT GCTTCTCAA 180
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTAAACCCG CGCGTTTACC 300
 TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60
 GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATC TTTCTTTGTG TTGCTTTTA 120
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180
 ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CGnACTACCA TCGACGCTAA 240
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300
 GACATATGAA TGTrAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360
 C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTTCACCT CGCCAAGCCA 60
 TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACTTCGC CAAGCCATTT TnCTTTGTGT nTACTnT 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAC 120
 GGAGGAAGAG GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240
 TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300
 TTTTACAAC TATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60
 AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120
 ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180
 GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240
 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA 300
 ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA 180
 5 AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240
 GTTnCATtGA AGTGTtTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTC TTGGACTGTG 300
 CATTtGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360
 10 GCTGAATGGC TtTnGnTGAAT GAATT 385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 180
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300
 CTTTCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60
 AGGTGTTATG AATGGCATAc ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120
 CAGAAGCAAG TGCGCATGCA TnACGCCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

TTTTGAGCGG CAAAACTTT GnCAG

385

(2) INFORMATION FOR SEQ ID NO: 4303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTTAAACGCA | 60 |
| | GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT | 120 |
| | TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGAC ACGTCATCTT TAACTTAATC | 180 |
| 20 | GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA | 240 |
| | GATTTATGGG CACTTAAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA | 300 |
| | TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA | 360 |
| 25 | CCAAGCCTTG TCCC | 374 |

(2) INFORMATION FOR SEQ ID NO: 4304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

| | | |
|----|--------------------------------------------------------------------|-----|
| 40 | AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA | 60 |
| | ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA | 120 |
| | ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAT TGGCTATCAC CCTATCGCTG | 180 |
| 45 | GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGTTGTA | 240 |
| | TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA | 300 |
| 50 | TTAAAACAAA CGTT | 314 |

(2) INFORMATION FOR SEQ ID NO: 4305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

(2) INFORMATION FOR SEQ ID NO: 4306:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CGGTGATTAT 120
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360
 GAAnAGATGG TCAAATTT 378

(2) INFORMATION FOR SEQ ID NO: 4307:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGAATTGGGT ATTCTTCCAA AATTATATGG ACCTTGCAGG ACTCGAACCT GCGACCGAAC 60
 GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

55

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240
 GATCGAACCG CTGGACCTCC TGC GTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300
 5 CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA 60
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTC CAATTAAGTTT CATTAAGTTT 120
 TTCTTCAGAC CAATAATAAC CTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTAC TTAAATATACG 240
 25 TGTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360
 30 CAATCCTATT GGATGTCCCA AnAATTGTAC GACCAACACC 400

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60
 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120
 45 GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCAATTTG ATGACAATGG 240
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300
 TTCACACTAA TCAATGGTGG CAAAGT 326

(2) INFORMATION FOR SEQ ID NO: 4310:

(A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG 60
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300
 TCGGATCACT TTT 313

20

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

30

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120
 35 TTGGGAAGTG CTTTTTTTTA GGTCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180
 TATTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240
 TGGTTGTCTT CnTTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300
 40 GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TCnATAGACC 360
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

40

(2) INFORMATION FOR SEQ ID NO: 4312:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

55

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180
 5 ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240
 CTTTAAATA ATTAACATCAT TGTCTGCnAA ACGTTTTcNT TTATAAAAAG ATTAAACGCG 300
 TTATTAA_nCT GTGGAGTG 318

10 (2) INFORMATION FOR SEQ ID NO: 4313:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC 60
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGA_nG GAGTCGAACC CCCACGCCGT 180
 AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240
 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGC_n 300
 30 AATGG_nTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAAC 60
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180
 50 T_nCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300
 GGCCATTTGA ACCGGTGGTT TCACATCGGT CATTT_nCCGT AAAAG_nCCAT TCCATG 356

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA | 60 |
| | AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT | 120 |
| 15 | CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA | 180 |
| | TGTAGCGGAA GGnATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA | 240 |
| | TTGGTGTAC AATTATCCTT GGnGGCCTT GCATATTCnG GGTGTAGGG AATCAGGTCC | 300 |
| 20 | GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT | 360 |
| | TGCCTCAGCG GAGGACACGC | 380 |

(2) INFORMATION FOR SEQ ID NO: 4316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT | 60 |
| | TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT | 120 |
| | GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT | 180 |
| 40 | ATTCTTTGTC CGTTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT | 240 |
| | TAACCTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT | 300 |
| 45 | TGTTGTCCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AACTTATAA TCCACACCCT | 360 |
| | GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn | 400 |

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60
 5 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTA ACT TATAAGCAAA 120
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360
 15 CCGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4318:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGA ACT TCCTCTTTCT 60
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTCTGGTC 120
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTGAT TCACCTGTAC 180
 TAATAATTTC TCCAGTTAAT GGATTTTTTA GTGTTGGCGT CGTTATTGTC TTCTCACCTn 240
 35 TTTGTCCTTC TCTTGTA ACT TTTTCTGTCC CCGTGCTAAA TnCGGATTAA ATTACGGTCT 300
 TTCTTGAAGG AATCTCTTC 319

(2) INFORMATION FOR SEQ ID NO: 4319:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

50 AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60
 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTTCACTTCGC CAAGCCCATC TTTcNTTGGn 360
 5 GTTTGCCT 368

(2) INFORMATION FOR SEQ ID NO: 4320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
 20 TCCTCTCCTT CGGCTCTCGC TTAATCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTACTTTT 180
 TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240
 25 TCTACTCTAG CGGAANTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

(2) INFORMATION FOR SEQ ID NO: 4321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120
 ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 45 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAACCTAAG CAAAAGTATT CAGATGCCTC 60
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA 120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG 180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAnGG AGCATCGAAA 240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC 300
CACGATCGTT TTGATGCATT TCAGTTCGGC 330

(2) INFORMATION FOR SEQ ID NO: 4323:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTMTA GCACTGTTTT GTCGTATTTT 60
TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA 120
CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA 180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA 240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTC 300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG 337

40

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA 60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG 120

55

GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAAGTGT ACCTGAACTT 60
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120
 TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240
 25 AGCACACGGT TTCAGGTTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTTCCCTC 300
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60
 40 CACTTTTTCG CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180
 45 AGACATATGA ATGTAAATTA TACATTCAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300
 50 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAGA CGATATACTA | 60 |
| 10 | CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT | 120 |
| | AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA | 180 |
| | GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA | 240 |
| 15 | TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT | 300 |
| | TTTGGTTnCA G | 311 |

(2) INFORMATION FOR SEQ ID NO: 4328:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

| | | |
|----|-------------------------------------------------------------------|-----|
| 30 | TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT | 60 |
| | CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT | 120 |
| | TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC | 180 |
| 35 | CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA | 240 |
| | CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG | 300 |
| | TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA | 340 |

40

(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

| | | |
|----|-------------------------------------------------------------------|-----|
| 50 | AATCCATAGC GAAATGTATA CCATCACCCA TCGTCCTTC TAAAGGTAAA TCTCTACCTT | 60 |
| | TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA | 120 |

55

TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240
 CGCCTGATTG TCTAGCACGT TCATAAATAG TTAAGTTCTT 300
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120
 GATTCGAACT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180
 ACCCCTCCAT AAATGGTGCG GGCnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA 300
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60
 40 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180
 45 TTGTTATTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240
 AGTCATCATA TGCAGGTGGA TTAAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300
 GGATAGCCGG ATGGnTTAAA TTGTTAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360
 50 GTTAAAACG TCACGACTT TGTTTAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

(A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC | 60 |
| | TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT | 120 |
| | AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT | 180 |
| 15 | TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTGCA GATAACTGGC TAGCACCGAA | 240 |
| | TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTTATTTTA CAAGGAACAT | 300 |
| | TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTAAAA CCATTATTAC | 360 |
| 20 | CAGGAT | 366 |

(2) INFORMATION FOR SEQ ID NO: 4333:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT | 60 |
| 35 | CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC | 120 |
| | ACCCCAACTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC | 180 |
| | CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA | 240 |
| 40 | CCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCCTGA | 300 |
| | CTGAGAATTG GAAAAAGCT TGTTGACAAG CGCnATTTTC GTTCCATGCA ACTGACTGCC | 360 |
| 45 | AAGAGAACHT CGTGAGAGCn ATGAAGAAGA TTGGATTGTA | 400 |

(2) INFORMATION FOR SEQ ID NO: 4334:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60
 GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AACTCTTTA 120
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240
 10 TGTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCCGCCA TCTTCTGnAA 300
 GAAGATGTT 309

(2) INFORMATION FOR SEQ ID NO: 4335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60
 25 ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAAAACGAT 180
 30 TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GnCTCAGCTT 240
 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

(2) INFORMATION FOR SEQ ID NO: 4336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 45 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATT AAGTTGGGCAC TCTAAGTTGA 120
 50 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180
 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240
 GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

(2) INFORMATION FOR SEQ ID NO: 4337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT 60
 TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCTAAAG 120
 AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT 180
 CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCATTATTT 240
 TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AnTGGCTnCT 300
 CCCATCAGAG CTCAGCCTTA ACGA 324

(2) INFORMATION FOR SEQ ID NO: 4338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG 60
 ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAATT TGATTCCGGTT GTTTGCTCAA 120
 TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA 180
 AGATAAGTCT AACAAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT 240
 ATTGGTAAAA ACACCCCGAG CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC 300
 TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT 360
 GTGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT 399

(2) INFORMATION FOR SEQ ID NO: 4339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TGCGCTCTAA CCAGCTGAGC 180
 10 TATAGGCCCA TTTnTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240
 GTTATTCCGC ATCTTCTGAA GAAGATGTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300
 AGCCGCACCT TCCGGATACG GCT 323

(2) INFORMATION FOR SEQ ID NO: 4340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

25 GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTCGAT TGGAATTTCT 60
 CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC CTCCATTCAG 120
 30 TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180
 TACTAAACGC CCTATTCAGA CTCGCTTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTAACGGG 300
 35 CTCTGAACTA ACTTGGTAAA GChCCGGTTT nCnGGTCCAA TTTT 344

(2) INFORMATION FOR SEQ ID NO: 4341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

45 TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

15 AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC 60
 CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA 120
 CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC 180
 20 TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAngA GCTTAACTTC TGTGTTCCGC 240
 ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 300
 TCAAAACTAG ATAGTAAGTA AAAGTGA 327

25 (2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

35 ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA 60
 CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC AACTGTTGA 120
 40 AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTTCA GATTGTCACC TTTAAAATAC 180
 GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA 240
 CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT 300
 45 TCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT 360

(2) INFORMATION FOR SEQ ID NO: 4344:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

5 ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60
 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120
 GACGGCTAGC TCCTAAAAGG TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180
 10 GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240
 CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACTT 300
 TATGGGATTT GCT 313

15 (2) INFORMATION FOR SEQ ID NO: 4345:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

25 ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60
 AATAGTTTTA CTTTAAGTCC AGCATTCACA AAAAGTGCTG CCAGTTGAGC GCCCATTTGTG 120
 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180
 30 ATAAGATAAC CATTAAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240
 CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT 300
 35 TTTTA 305

(2) INFORMATION FOR SEQ ID NO: 4346:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60
 TTTTAAGCTT GAATTAAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TGTAGCAAGT TGCTCAAATT 180
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTCGGA TGAnCAACGC CAACCAAAT 240

55

AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

5 (2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

15 TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60
 ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120
 20 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300
 25 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATTT 60
 TTTAGGTCTC GTAGTGTAGC GATTAACACG CCTGCCTGTC ACCCAGAGAT CGsGGGTTCG 120
 40 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTTT TCGTTTAAT 180
 ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTCGTCCA 240
 45 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTn 300
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

5 CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60
 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120
 TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC 180
 10 CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCG AACCTCTGAC CCTCTGATTA 240
 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300
 CGAACCAACG AGTGACGGA 319

15 (2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

25 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAATGGTG GAGAATGACG 60
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180
 30 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300
 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

35 (2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120
 50 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG 180

55

ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300
TGACC 305

5 (2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTTCATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60
 CTTTAAAACC TGGCTTCTTT GGCTTTTTCG ATATAATGTT GCGATTGTTC TATTGTAAAT 120
 20 ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180
 GCAATCATTT CTTCTAAAAA TGCCTCATTT GAACTTGCCT CTTTAGGTAC AGCATGAGGC 240
 CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTCTCAG CTAAACGATT AGnCACTTTC 300
 25 AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60
 TCCTAAGTCT AGTGCGTCTG CCAATTCGCG CACACCCGCA AATGGTGAGC CATAGAGGAT 120
 40 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240
 45 CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300
 GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360
 CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

50 (2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa | 60 |
| 10 | CGACAACTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT | 120 |
| | CTCAAATTTT CTACGACCAC GACGGATAGG GACCGAACTG TCTCAGCAGC TTCTGAACCC | 180 |
| | AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA | 240 |
| 15 | GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAAC TCTTGGGGGA | 300 |
| | GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG | 360 |
| | GAAACCA | 367 |

20

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| | (A) LENGTH: 313 base pairs |
| | (B) TYPE: nucleic acid |
| 25 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

| | | |
|----|--------------------------------------------------------------------|-----|
| | GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACC | 60 |
| | TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT | 120 |
| 35 | TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT | 180 |
| | TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT | 240 |
| | AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACCTT | 300 |
| 40 | GnCATTGTCT GTT | 313 |

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:

| | |
|----|----------------------------|
| 45 | (A) LENGTH: 335 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

| | | |
|--|-------------------------------------------------------------------|----|
| | GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT | 60 |
|--|-------------------------------------------------------------------|----|

55

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180
 GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 240
 5 ATGAGGTTAA TAGGTTCGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT 300
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

(2) INFORMATION FOR SEQ ID NO: 4357:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGn 60
 nGAACCTAAA AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120
 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 300
 AGAG 304

30 (2) INFORMATION FOR SEQ ID NO: 4358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

40 ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60
 TAGATGCTAC TGTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120
 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTAA GCATTAGCAA 180
 45 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240
 AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTGAT AACATTCAnn TCGACTCAnC 300
 50 AG 302

(2) INFORMATION FOR SEQ ID NO: 4359:

(A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGCGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240
 TCCCAAGGGT TGGGCTGTTC GCCCATTAAA GCGGTACAnG GCTGGGTTCA GAACGTCGTn 300
 AGAAAGTTTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

20

(2) INFORMATION FOR SEQ ID NO: 4360:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60
 GGTGTGTACA AGACCCGGGA ACGTATTACG CGTAGCATGC TGATCTACGA TTAGTAGCGA 120
 35 TTCCAGCTTC ATGTAGTCGA GTTGCAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180
 ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240
 AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300
 40 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

(2) INFORMATION FOR SEQ ID NO: 4361:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA 60

55

CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT 180
TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240
5 TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300
GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360
10 TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420
TCGC 424

(2) INFORMATION FOR SEQ ID NO: 4362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60
25 CGTGACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTTGGTA AAGAAACGCA 120
ATTnAnTCGT TATTTCCGAC AAGAACGTAA CAATACTACA TACAACTTAG CACCATGAAT 180
30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240
AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300
TGGACAGCAG ATTCCA 316

(2) INFORMATION FOR SEQ ID NO: 4363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120
50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180
AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240
55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

(2) INFORMATION FOR SEQ ID NO: 4364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

nTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG 60
 GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA 120
 GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG 180
 TGTACCTCAC GCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA 240
 GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTTAGTACGT GGTATATATC 300
 GTTCCAAAAA CGT 313

(2) INFORMATION FOR SEQ ID NO: 4365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

AACCATTCTGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC 60
 GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC 120
 TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG 180
 CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn 240
 CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn 300
 AGTCATTTTC 310

(2) INFORMATION FOR SEQ ID NO: 4366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60
 AACTTCTATT GATGGCCTAA CTGCCTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120
 5 AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180
 GTTACAAATT ATTTCAGGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC 240
 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300
 10 ACATTAA_nGG TATTAATTCT TAAACCACAT AAACGTCAA GAATGGTAAT ACAATCACGG 360
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG _nAATTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 4367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCTT ATTTATCAAC GGTATATGAA 120
 30 GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG 180
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240
 CGATGTTACT CGC_nATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACG_nATG_nC 300
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120
 CAATGGCAAC TTCTGTACCT GT_nCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180
 GTGCATCATT TACACCGTCA CC_nCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

GTTTTGC

307

(2) INFORMATION FOR SEQ ID NO: 4369:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

| | | |
|----|-------------------------------------------------------------------|-----|
| 15 | TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG | 60 |
| | CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTTCGAAAT | 120 |
| | CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA | 180 |
| 20 | TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT | 240 |
| | CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACAYTAGC GATTATTTCT | 300 |
| | TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA | 360 |
| 25 | TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA | 396 |

(2) INFORMATION FOR AN UNSEQUENCED SEQ ID NO: 4370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

| | |
|-------------------------------------------------------------------|-----|
| CAGTAAGATA ATTTTCAATT AGAAAATATC TTAGTGCTGT TCTCTATTTA TACAATACTT | 60 |
| CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT | 120 |
| GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTACATA | 180 |
| CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTTAATTC AATAATTTGA | 240 |
| ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTArTGAA | 300 |
| GTGCCTTATG TATAA | 315 |

40

45

(2) INFORMATION FOR SEQ ID NO: 4371:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60
 CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120
 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180
 10 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAAATCA CCAGGGnCAC 300
 15 CAAAATTTTT ATCGACGGCn TG 322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CCTAAGTCTA GTGCGTCTGC CAATTCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60
 CGAACCTCTG ACCCTCTGAT TAAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120
 30 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTTCGnA 240
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

(2) INFORMATION FOR SEQ ID NO: 4373:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120
 AGTCATTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

55

TCAATTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360
 5 GGNGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60
 20 TACTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTCT CGAATGGAAT 120
 CTCTTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACTT 240
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300
 nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTGCGGAAA CCGnAGCTAA 120
 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180
 45 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAAC T GAGACACGGT CCAGACTCCT 300
 50 ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT | 60 |
| 10 | AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TCGGATTCCT GAAGTATTGT | 120 |
| | CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTGCTCT | 180 |
| | CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT | 240 |
| 15 | GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA | 300 |
| | CTTAA | 305 |

(2) INFORMATION FOR SEQ ID NO: 4377:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

| | | |
|----|-------------------------------------------------------------------|-----|
| 30 | AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC | 60 |
| | AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT | 120 |
| | CCCCCATCG ATTAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC | 180 |
| 35 | CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG | 240 |
| | GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT | 300 |
| 40 | TCTCACTTCT AAGCGCTCCA CATG | 324 |

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

| | | |
|----|-------------------------------------------------------------------|-----|
| 50 | CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA | 60 |
| | AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT | 120 |

55

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300
 5 GGAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAntC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

ATAAAATATA TCACTTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60
 TTGTGACTGA GATGAACTTT TATGTCTTAG ACACTACAAC ACTATATTGG CAGTAGTTGA 120
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240
 GTGTACTCAT GTTGCGATTA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300
 TCGCTACATA ATCCATCCAT TAGGTCGTTC CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60
 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120
 45 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180
 CTGTGTTAAC TGGTCGTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240
 AGATATGCTA TTATTCATGG AAGATTAGTG CTTTCATCTTT TTTACCCCAA TATTTTATAA 300
 GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360
 ATn 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAAGTTG ACTTTnCGAC AATTGACTGT nCATTTTTGCA TAGTTGTATG 60
 nCTCCATTnC GTAATTATTA GATTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT 120
 ATAGTTAGCG TATTTCACCC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATT 180
 TTAAGTAAAT TAAGGAATCT ATAATGTTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA 240
 CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTGGGAC 300
 CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG 360
 GCCGTTGTCA CTTAACTTCT GTTTTCCGA TGACAGCTTC 400

(2) INFORMATION FOR SEQ ID NO: 4382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTTAC TGACGAATAC TGGCAATGAC 60
 ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC 120
 CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTCAG 180
 TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT 240
 TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT 300
 AGGG 304

(2) INFORMATION FOR SEQ ID NO: 4383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60
 GGCGGTTTGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180
 GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300
 AGTTGGTA 308

(2) INFORMATION FOR SEQ ID NO: 4384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTTGAGAGTG TCATTGGCAT TTATTACACT 60
 25 ATCTCCAACCT CCTAGTGGA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGKAGCTA CACCCTTTCC 240
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300
 TTTAGAnAT 309

(2) INFORMATION FOR SEQ ID NO: 4385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60
 45 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTCGTAGCC GAnAACAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

(2) INFORMATION FOR SEQ ID NO: 4386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

| | |
|-------------------------------------------------------------------|-----|
| TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA | 60 |
| ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA | 120 |
| TGGCAAGGTC ATCTTCAAAA TGATTCGATT CAAGTGAAG GCATATGACG TCTCATCACT | 180 |
| ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC | 240 |
| CATTCGCGGC AATCTCGGTh AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT | 300 |
| TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG | 360 |
| CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTCnGGCAT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

| | |
|-------------------------------------------------------------------|-----|
| TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA | 60 |
| TTACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAAA TAATTTTACA | 120 |
| GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG | 180 |
| CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTnC | 240 |
| GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA | 300 |
| TGGATGACGA | 310 |

(2) INFORMATION FOR SEQ ID NO: 4388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA 60
 5 CTACTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120
 TGTTAGCGAT nCATAACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180
 10 TGAAC TAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240
 TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300
 TTTGGCGTGG 310

(2) INFORMATION FOR SEQ ID NO: 4389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA 60
 25 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120
 TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180
 30 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA 240
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300
 35 CA 302

(2) INFORMATION FOR SEQ ID NO: 4390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60
 50 ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

TnCCTTACCA CCTATAATCG nTTAATCGTG GGG

333

(2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

| | |
|--------------------------------------------------------------------|-----|
| AGTGCGTTTG TGCACAnACT TGA CTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG | 60 |
| GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA | 120 |
| TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG | 180 |
| CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT | 240 |
| ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC | 300 |
| AACCAT | 306 |

(2) INFORMATION FOR SEQ ID NO: 4392:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

| | |
|-------------------------------------------------------------------|-----|
| TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTTATT AGGACATATA AATTCATCAT | 60 |
| TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT | 120 |
| TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAAATCA TCTATAATAG | 180 |
| CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAAATAAC | 240 |
| CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT | 300 |
| GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTnGCCnC AATTnGTAAA TGGAA | 355 |

(2) INFORMATION FOR SEQ ID NO: 4393:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTTTCAGG TTTCTTCTTT GCATTGTTGGTG 60
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTAnTAAC GATAATGGCG 360
 15 nnGG 364

(2) INFORMATION FOR SEQ ID NO: 4394:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

25 GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60
 CGGCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120
 30 GTCAATCGGT GGACGGGATT CTCACCCGTC TTTGCTACT CACACCGGCA TTCTCACTTC 180
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAACGCT CTCCTAnCAT 240
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300
 CATGTnCACT CGACT 315

(2) INFORMATION FOR SEQ ID NO: 4395:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCCAA TGGGTATTGA AATTGAATGG TGGGnCCCTGA AnTGGACTCG AACCACCGAC 60
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120
 ACAAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

55

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300

ACCGGCTTCG GGTGTTACAA AC 322

5 (2) INFORMATION FOR SEQ ID NO: 4396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120

20 GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA 180

GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTG ACAATCGCTT 240

GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300

25 CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTG AAAGCTACAA CATTCTATA AAATTTTCA 60

40 ATAACAATTG CGCCACTAAA ACTCAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120

GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180

GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACTGCA GCAACAAGCT GAATTACATA 240

45 AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300

TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360

GCAGATGCCT GGCCAGG 377

50 (2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

| | | |
|----|-------------------------------------------------------------------|-----|
| | TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC | 60 |
| 10 | GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG | 120 |
| | GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC | 180 |
| | AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT | 240 |
| 15 | AAGCAACTAA TATCATTGTC AACCATTAAT TTACCGTTAC CAACCAATAT ATGGTGATGA | 300 |
| | TCnATCCTTC CTC | 313 |

(2) INFORMATION FOR SEQ ID NO: 4399:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

| | | |
|----|-------------------------------------------------------------------|-----|
| 30 | TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA | 60 |
| | TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA | 120 |
| | AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA | 180 |
| 35 | TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA | 240 |
| | AAAATTTTIG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT | 300 |
| | GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAGA | 360 |
| 40 | ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT | 400 |

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

| | | |
|--|------------------------------------------------------------------|----|
| | CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT TTCGTCAGAT TCAAACGTTT | 60 |
|--|------------------------------------------------------------------|----|

55

AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180
 TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240
 5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 300
 ArATTCAAAC GtTTTCaCTT CGGCCAAGGC ATTTTTCTTT GTGGTTACTT TTTAATTGG 360
 10 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409

(2) INFORMATION FOR SEQ ID NO: 4401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60
 ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120
 25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180
 TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240
 TGGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300
 30 TCCATATTTC C 311

(2) INFORMATION FOR SEQ ID NO: 4402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60
 45 AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120
 TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180
 AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTAAAAAATT 240
 50 TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAACAGA AAATTAAAGC 300
 AGGTCCATGT nAAGTGTTGG CGGGnCGCAT 330

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

| | | |
|----|--------------------------------------------------------------------|-----|
| 10 | TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC | 60 |
| | TTTGGGCCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT | 120 |
| 15 | TACTTTTTTCC ATCGATAAGC CATACTCTG GATGATACAT ATGATGCCCC ATCGCAGACC | 180 |
| | AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT | 240 |
| | TTTGAGGTGG TACTTGATAT AAATTTTCIT CTCTAAAATA TTCATTTAAA ATGCGTTCGA | 300 |
| 20 | TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTG | 340 |

(2) INFORMATION FOR SEQ ID NO: 4404:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

| | | |
|----|--------------------------------------------------------------------|-----|
| 30 | TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA | 60 |
| | CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAAATTG GCATTCCGAG TTTGTCTGAA | 120 |
| 35 | TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AACAGTGCT CTACCTCCAA TAATCATCAC | 180 |
| | TTGAGGCTAG CCCTGAAAGC TATTTCTGGGA GAGAACCAGC TGATTTCAG GTTCGATTGG | 240 |
| 40 | AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC | 300 |
| | TGCCATT | 307 |

(2) INFORMATION FOR SEQ ID NO: 4405:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180
 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300
 CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAACACG TATGGAAGAC GAACTTGGAG 60
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120
 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180
 AACTTTCCTG AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300
 ACnChAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCATC ATAAAATAGG TGGACAGGAA TATCAACCTG 60
 TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120
 CTCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180
 CACCGGCATT CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240
 AGAACGCTCT CCTACCATTG TCCAAAGGAA TChCACAGCT TCGGTAATAT GTTTAGCCCC 300
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG 60
 TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC 120
 ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA 180
 TGTGTTAGAT ATTACAGCAG CACATTTATC TCGCCAAAGT CCCAGCTGTC GATAAAGGTT 240
 GAAACTGAAA AACGGATTTTC TGGATTTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG 300
 AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAATTGG AATCCAAATC nnTTACCAGG 360
 TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC 393

(2) INFORMATION FOR SEQ ID NO: 4409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC 60
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTTC ACTTCGCCAA 120
 GCCATTTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT 180
 TGCCTTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 240
 AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCCTG ACTTGTGGAC AATCGCTTGG 300
 CnTCTnTCCT CTCCTTCGG 319

(2) INFORMATION FOR SEQ ID NO: 4410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAATACGC CTAACCTCGT TAACTTTTAA 60
 AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGT TTGGTAA 120
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAACGTGACGA CCAGTTTTTC AACTGAGCAC 300
 10 AATTGTGCAC ATCGATTGGT GACAG 325

(2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120
 TGAAATGACG ATAGAGTCAG TATTAACCTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTAA TTGGCCATTC GGGTAAGTTG 300
 TCCGACCATT GCCAAGTGGG TGATGAGTTn AGGCCAGTCC GCAAAGATT GGGAAAGTAG 360
 TCCGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

35 (2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60
 CCCGAGCACA TTATTTTCATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120
 50 GAATGATAAT CGAACGTCAT ATTTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAATTA AACATAACCA TCACCATTTA 240

55

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTnTGAAT ACCCGGAGTT 360
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

15 TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACnCGTTG CGCTCTTTTC TCGTTTCGTC 120
20 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTnTACTTT TTATTTTGAC 180
GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTnACTCTA 240
GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC 300
25 TTGCGTCCTT nCCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACnAGTA CCGTGAGGAA 60
AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120
40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT 180
TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240
TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300
45 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60
 TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT 120
 CTCAAATGCG GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA 180
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTh 300

(2) INFORMATION FOR SEQ ID NO: 4416:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180
 30 CATATAAGAT GATTTTAAAC ATCATCTTTG GATGATAGGA TGTTGCGCCA CGATGATGTC 240
 TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

(2) INFORMATION FOR SEQ ID NO: 4417:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA 120
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTC AAGCAAATA 240
 TGTAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

55

GTTTGGTGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 4418:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

| | | |
|----|--------------------------------------------------------------------|-----|
| 15 | GTATTTACAA TCAAACCTAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT | 60 |
| | CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG | 120 |
| | GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG | 180 |
| 20 | CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTTAG TAACTCATAC | 240 |
| | AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG | 286 |

(2) INFORMATION FOR SEQ ID NO: 4419:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

| | | |
|----|-------------------------------------------------------------------|-----|
| 35 | CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT | 60 |
| | CCTACCATTG TCCAAAGGnA TGChCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT | 120 |
| | TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA | 180 |
| 40 | AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG | 240 |
| | GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG | 300 |

(2) INFORMATION FOR SEQ ID NO: 4420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120
 AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCCG 240
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAAcT ACGAATCGAA GCCCCAGTAA 300
 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

10 (2) INFORMATION FOR SEQ ID NO: 4421:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCTC 120
 25 AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT CCATTCAGTG TTACCTGAAC 180
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240
 TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTACTGCTTA ACCTTGCATC AAATCGT 297

30 (2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60
 ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTCGT 120
 45 GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240
 CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCAn CAATAGAATG 300
 50 ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACTAT CAAGCTTTGA 60
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240
 ACAACGGTTG GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGGTAGT T 291

(2) INFORMATION FOR SEQ ID NO: 4424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnC GTTCCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTTTTATn CAGTAATGGG 180
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240
 GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

(2) INFORMATION FOR SEQ ID NO: 4425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTTTTGCGA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120
 ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300
 10 CCATThTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

(2) INFORMATION FOR SEQ ID NO: 4426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAATTACG GATCATGATG 60
 ATTTACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTGAG 180
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240
 30 ATAGCGACTC AGATTGAGAT AGCGATTGAG ACTCAGACAG CGACTCAGAT TC 292

(2) INFORMATION FOR SEQ ID NO: 4427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60
 AACCAGCTAT TTCCAGGTTT GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120
 45 TTTCACGTA ATCGGTTCGG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180
 TAGATCACCT GGTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240
 50 CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300
 ATTCTAn 307

(2) INFORMATION FOR SEQ ID NO: 4428:

(A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60
 TTTTTCAGCAG CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTCAT ACGAGATGGT 120
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180
 15 ATCTTCTTCA GGGACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAAT GATGATTATT ACACGTnACT 300
 AATTGGTTTA CACCAGGTGG AnAATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

20

(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA 60
 CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120
 35 TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180
 GTGCACATTA TTAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTCTTGT 240
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300
 40 GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTCGGCTCT CGCTTACTCC ATTTAGCTCC 360
 ACTAAACTCG TCGGGCCCTT CCCGTTTCGGC AGATCCAACG 400

45

(2) INFORMATION FOR SEQ ID NO: 4430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

55

ACCATTGACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180
 5 ATCGATAGCG TTTTGCGCAA ATTCTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

20 TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180
 25 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAAC TTTGA GCGCCTCCGT 240
 TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

40 TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT 60
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180
 45 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300
 50 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

| | | |
|----|--------------------------------------------------------------------|-----|
| | CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT | 60 |
| 10 | TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC | 120 |
| | AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAG AACTCGGCAA | 180 |
| | AATGACCCCG TAACTTCGGG AAAAAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC | 240 |
| 15 | AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT | 288 |

(2) INFORMATION FOR SEQ ID NO: 4434:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| 20 | (A) LENGTH: 336 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

| | | |
|----|--------------------------------------------------------------------|-----|
| | GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC | 60 |
| 30 | AATCGAACCT GGAGATAGCT GGTCTCTCTn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT | 120 |
| | GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCCCT CTCGGGTTAC CAATTTCAGA | 180 |
| | CAAACCTCCG ATGCCAATTA AATTTAACTT GGGAATTCAG AACATGGGTG ATnAAGTCCG | 240 |
| 35 | TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA | 300 |
| | AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT | 336 |

(2) INFORMATION FOR SEQ ID NO: 4435:

| | |
|----|-------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 304 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 45 | (D) TOPOLOGY: linear |

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

| | | |
|----|-------------------------------------------------------------------|-----|
| 50 | ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG | 60 |
| | GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG | 120 |
| | GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC | 180 |

55

AATCATTGGC TGCCTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300
ACGA 304

5 (2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAAATAAC CGAAGAGTTT TGAATCATTG TTA AAAATGG AATTAnAGTT 60
CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120
20 ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTCA TATGGTCTTC CTTCAATTCTC 180
ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT 240
TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACTTCT 300
25 TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60
TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120
40 TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180
AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTTACA AGGGGGAnAA 240
45 AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300
GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60
 CATAAACCTT GnAAACGGCA ACATTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC 120
 ATTATGATCA ATATCATGCC CAATTAACCTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180
 10 ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240
 ATCTTTATTA ACAATTGCTT CATCATTAAT ATGTGAGATT AAATCG 286

(2) INFORMATION FOR SEQ ID NO: 4439:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 240
 30 GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTTCCTCh 300
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT TCTCGTTTCG 360
 35 TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT 394

(2) INFORMATION FOR SEQ ID NO: 4440:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60
 GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCTATG 180

55

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn

295

(2) INFORMATION FOR SEQ ID NO: 4441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60
 CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120
 TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240
 TAAATAAACA TTCAAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300
 TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

(2) INFORMATION FOR SEQ ID NO: 4442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCAC 60
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120
 CGTCATTGCT CAAATCATTC ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTCGCA TCGTTAACAT 240
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT 300
 GTATCTTGGA TGC 313

(2) INFORMATION FOR SEQ ID NO: 4443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

5 AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTC 60
 CAGTCTTTAA AAATAGATTG TTTATTTTAA GAATTATTTT TGAATAATTG AATTGCTTTG 120
 TAGCCAAAAT ATGACGTTCG ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240
 10 CTGAAACCCC ATTCCCTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300
 ATACGGnCCG TAGnCCATTC CATTTCaATT CTTTTC 336

(2) INFORMATION FOR SEQ ID NO: 4444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

25 CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60
 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTCTGAAGGG TGAAATTGAA GCGGTACCTG 180
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240
 ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300
 35 TCCGTGTCCA GTTGAACCAT TATGGAGGAn TThAAAAAGT ATGTTAAGGG ACCTGGGAGT 360
 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

(2) INFORMATION FOR SEQ ID NO: 4445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

50 TACGCCCACG ACGGATAGGG ACCGAAGTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60
 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

55

CACTAAGTCC GTGCTTTCGA CCCTGACTAC GGACTTGThA GGTCTGCGGC ATTCAAGCTT 300

CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTTG 339

5 (2) INFORMATION FOR SEQ ID NO: 4446:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTGAAAAT GTCACCTTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60

CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120

20 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT 180

CATTGTTAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240

ATAAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300

25 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60

40 TTTTATTTCA GTCAACTACT AACAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120

ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180

TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240

45 GTAAAAAATG AACGATCAAT GGTnTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

5 GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60
 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120
 CCCCAGTACA TTTTCGGCGC AGTGTCACCT GACTAGTGAG CTATTACGCA CTCTTTAAAT 180
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT 240
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300
 GA 302

(2) INFORMATION FOR SEQ ID NO: 4449:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

25 CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG 60
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTCGAA TGTTTAGTAA 120
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180
 30 TACAAAACAA TGA_nACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300
 35 TCGCGGATGA CCTAATA_nCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

(2) INFORMATION FOR SEQ ID NO: 4450:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

45 GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTG_nA TCAAGGTACA 60
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAA CAATACTTTT ATAGGGCAAC 120
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180
 AGATCGTCG_n TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAGCT 240

55

GCTATACGGT AGAACGACTT ATTCCC

326

(2) INFORMATION FOR SEQ ID NO: 4451:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

15 GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60
 TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120
 TCAACAACCTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA 180
 20 AGACAACCAA GCCCAATAAT GGA CTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT 240
 TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTA AACCAT 300
 GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA 360
 25 TAAAGCGGGG GGCAATTGGG G 381

(2) INFORMATION FOR SEQ ID NO: 4452:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT 60
 40 CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC 120
 TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 180
 CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA 240
 45 AATAAACATT CAAACTGAA TACAATATGT CACATn 276

(2) INFORMATION FOR SEQ ID NO: 4453:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTTAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60
 5 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120
 AAATGCGCAG AGATATGGAG GAACACCAGT GAGCGAAGCG ACTTTCTGGT CTGTAACTGA 180
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AGTGGCTGCC AGCTAnACGC 300
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

(2) INFORMATION FOR SEQ ID NO: 4454:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

25 ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG 120
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180
 30 TAAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240
 TATTAATCTT GTGAGTGTTT TTTGGAACAC TAGCGATTAT G 281

(2) INFORMATION FOR SEQ ID NO: 4455:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

45 ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60
 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTTCTACT 120
 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 50 GCTTGcTCTT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60
 CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240
 nTCACTTCGC CAAGCCATTT TTCTTGTTT TACTT 275

(2) INFORMATION FOR SEQ ID NO: 4457:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120
 TTCGGTAAGC ACATCAGCGT CATTAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCGTCA ACATCACTCA GTGACTCAAC 240
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300
 AntGGAATCC GATTGTGCGT CAACATCTTT AAGTGGATTG AACATCTGCG TChATGCCAA 360
 AGnnGTGAAT CCGATTCACA AAGCACATCA GCATCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4458:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300
 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

10 (2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTTnACAATA 180
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240
 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

30 (2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT AAGTAAAAGT 180
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

50 (2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG | 60 |
| 10 | TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAATC | 120 |
| | AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC | 180 |
| | TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAAT CAACAAnCAT AACTTTCCnG | 240 |
| 15 | GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC | 274 |

(2) INFORMATION FOR SEQ ID NO: 4462:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| 20 | (A) LENGTH: 271 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GGCTGCTAAA AATCTTGGA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA | 60 |
| 30 | CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA | 120 |
| | TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT | 180 |
| | GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT | 240 |
| 35 | TGnTACACAA CAACCACTTG GCGGTnAAGC G | 271 |

(2) INFORMATION FOR SEQ ID NO: 4463:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| 40 | (A) LENGTH: 300 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

| | | |
|----|-------------------------------------------------------------------|-----|
| | GCGGCTCATC GCATTCATTT CTTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC | 60 |
| 50 | TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TCCTCTCCT | 120 |
| | TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC | 180 |
| | AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTAAnTTTGAC | 240 |

55

(2) INFORMATION FOR SEQ ID NO: 4464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGCGC ACTGTCTCAA 120
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180
 GAAAGACCCC GTGGGAGCTT TTAAGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360
 G 361

(2) INFORMATION FOR SEQ ID NO: 4465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAG TATAAATTCA 60
 ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120
 AAGGTGCTAT TCCTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGTGTTT TTTTnTTTT TT 292

(2) INFORMATION FOR SEQ ID NO: 4466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300
 10 AATAnTGG 308

(2) INFORMATION FOR SEQ ID NO: 4467:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGGAAGAC 60
 25 AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAAAGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

(2) INFORMATION FOR SEQ ID NO: 4468:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TGCGTCAAAG TCCAGCTGTC GATAAAGTTG 60
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240
 50 AACGATTAAC TGGTATTCCA GTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300
 ATATTT 306

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

GGTTTATTAA CAGCATTCTT ATCAGCATTT GTAAGTGTAA TTGTTTATAA CTCTGTGTG 60
 AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTC ACAAGTATTT 120
 AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTTCTT ATGCATTAGA TTTAGTCATT 180
 CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240
 ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTAAACnT TGGGnGCnTT TGCATTAATC 300
 CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

(2) INFORMATION FOR SEQ ID NO: 4470:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 60
 AATATATGTT AAGTGGA AAA GGATGTGGCG TTGCCCAGAC AACTAGGATG TTGGCTTAGA 120
 AGCAGCCATC ATTTAAAGAG TGCATAATAG CTCACTAGTC GAGTGACACT GCGCCGAAAA 180
 TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240
 CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300
 TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360
 GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

(2) INFORMATION FOR SEQ ID NO: 4471:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCATTTTtag AAATATTATC TTTTCCACAA ATCATTtGAT ATAAAGTGCG ATCATTtGCC 60
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTtT TGGCTAGCAC TTCGGGATAC 120
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTtGA AAATATCATT ATCTTGACCC 180
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCTCTC GTTTTtNCATG TACCGCGAGG 300
 10 CGTAAnCTTA AAGGGCCCAA GGnCG 325

(2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

(2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTt ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAAGaATA GATTGTCAAG CGCTCGCATA 120
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTtAAAT AAACATTCAA AACTGAATAC 180
 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTC CGAATATATC CTTAGAAAGG 240
 50 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTtA CGACTTCACC CCAATnCATt 300
 TGTCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

10

| | |
|-------------------------------------------------------------------|-----|
| TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG | 60 |
| AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGGC GCAGGCACAA TGGGCGCTCA | 120 |
| ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAANA CTATTAGATA TTGTAGTGGA | 180 |
| CAAAAACGAT CCnAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG | 240 |
| GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTACCAT ATGGTATTTT GATGTGCTTG | 300 |
| GTAAATGTGT GCTGTTTGAT ATCGA | 325 |

15

20

(2) INFORMATION FOR SEQ ID NO: 4475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

| | |
|-------------------------------------------------------------------|-----|
| TAAGTGGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA | 60 |
| CAATACATCT AGTATTATCT GGTATTTTGG ATCGTTATCC AAAGTTAAAT AATGATTATT | 120 |
| GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT | 180 |
| GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA | 240 |
| TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC | 300 |
| TGATATCC | 308 |

35

40

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

55

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120
 GGGTCTTTCC GTTCCTGTCTG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTACACCGA 180
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TGCGGGTCGG AACTTACnCG 240
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAAATGG TCCTCCACCT TGAGCTTCTT 120
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240
 GGAAnACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

5 GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60
 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120
 ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180
 AAGCGCATT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240
 10 TTTATGTCCC AGCCTGAGTT AATTT 265

(2) INFORMATION FOR SEQ ID NO: 4480:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

25 ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60
 ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACTTAA CTTCTTGTTT TTCCGATGAC 120
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180
 TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240
 30 ATATTCCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

(2) INFORMATION FOR SEQ ID NO: 4481:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

45 ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

55

(2) INFORMATION FOR SEQ ID NO: 4482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60
 CATCAAATTA TCGGTGCTAC TGtnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180
 ATGGGGATTC GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

(2) INFORMATION FOR SEQ ID NO: 4483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60
 TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180
 CATTTAGCTC TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240
 ACTTCGCCAA GnCATTTTTTC TTTG 264

(2) INFORMATION FOR SEQ ID NO: 4484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180
 nAAGCCTCTA GATAGAAAAA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240
 AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTGTGAC AGATTCCATA TCGTTCAACA TTTAAATAGA GAACTTAATA 60
 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180
 GATGGAAATA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAA GTCATGCTTT 240
 CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACCTTCTC GTGTCTCACC AGATTTAGCG ACTAAACTTG TAGACATACG 60
 TAAATCTGCT TTAATAAGTA ATTnATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGAnTTTGAG CGCCTTGCTT 180
 TACAGCATTC ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240
 TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTTCCTT CATATTTATT 180
 10 TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACTTC TTAATCTTAG TTCTTTTTTA 240
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTTCCCCA ATAGAATGAA TTAAACCTT 300
 CCGATTCCTT TTAAnC 316

15 (2) INFORMATION FOR SEQ ID NO: 4488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60
 TCAAAAAGTT ATAGAAGAAG CTACTAAAGT TAAACAGAG ATTGATACTG CCAGAAGATA 120
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180
 ATTAAACCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT 240
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300
 35 GACTCAA 307

(2) INFORMATION FOR SEQ ID NO: 4489:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60
 50 GTTCCCCAAT CATTAATTTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC 180
 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240
 55

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

(2) INFORMATION FOR SEQ ID NO: 4490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACC GGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCTGTC 60
 TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT 120
 TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180
 TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240
 CAGGTACTnA GTAACTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300
 TTCATTTGAC CGG 313

(2) INFORMATION FOR SEQ ID NO: 4491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT 60
 ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCAACA TGAGCCAGAA CGTGATGAAG 120
 TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180
 AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240
 AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnCh A 291

(2) INFORMATION FOR SEQ ID NO: 4492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAAACACT TTGCCCAACT 120
 5 TACACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAT GATATTTTCGC GATATGTTAA 180
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTCGATGG AATTCAGACA TCATCGTGGG 240
 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300
 10 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGcNT 400

(2) INFORMATION FOR SEQ ID NO: 4493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120
 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180
 30 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240
 ACGAATCATC TGGAAAGGTG AATCA 265

(2) INFORMATION FOR SEQ ID NO: 4494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60
 TAAGGAAGAG ATTTCCCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120
 ACATAATCTT TACGGTAACA TGGGTTcAGG AACAATCGTT ATTAAAATGA AAAACGGTGG 180
 50 GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG 240
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60
 ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAAGTGAAT AACTGCAGCT CAACGTGTTA 120
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180
 GCATTTAACA GCATTAAAC CAAGCGAAAC ATGANTTTAA CTGCAGATTA CACATGCCTT 240
 AGGAGCAAGC AGTGCA 256

(2) INFORMATION FOR SEQ ID NO: 4496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTC CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60
 TTCATCATTA TCTAATTAA AACAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AATATACCAA TATACTTTTT 180
 ATATCGTTTC GATTCTGAGT ATTCAGACG ATTTCTGCA TAAATAAAA CGTGTTTCAA 240
 GGCAATATAT TGCA 254

(2) INFORMATION FOR SEQ ID NO: 4497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGATATCTGA ATCCGAGTCG 60
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240
 TCACTGTnGG AATCTGAATC GCTATCTGA 269

(2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTCG AACCCGCGAC CCCAACCTTG 60
 GCAAGGTTGT ATTCTACCGC TGAAC TACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120
 CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180
 AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240
 CCAACTGAGC TAAATGGCTC Tn CAGGTGC CGG 273

(2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60
 TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120
 TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180
 TCAACGAAGG AGACAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240
 AGCAAGTGGA GGAATTCGAA GTTGTTCanA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300
 AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60
 5 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120
 ACTTAACTTT AATGGCGGTC GTCACATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180
 CCATTTATGC TGTAAAAGG CGGTATAGCT GATAAAGTAT GGCTGATTA CGGTGGCGGT 240
 10 AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAACT GGTATATGCA TTTATCTAAG 300
 CATT 304

(2) INFORMATION FOR SEQ ID NO: 4501:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

25 TTCCTTCATT CTCATAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60
 TCTTTAAGAA TCGATTTTGG TTCTTCATAT TTATTTTTTC TTTCGGATA ATCATCAAAT 120
 TTCTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTTGAGCA 180
 30 CAATCTTCGT TCTCAATAAG AATGATTAA ATCTTCGATT TCTTTATCTA AATGGACTAC 240
 CAATTAAATC TAT 253

(2) INFORMATION FOR SEQ ID NO: 4502:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

45 AGTTCGGTCC CTATCCGTCG TGGCGTAGG AAATTTTGA GGAGCTGTCC TTAGTACGAG 60
 AGGACCGGGA TGGACATACC TCTGGTGTAC CAGTTGTCGT GCCAAGCAT AGCTGGGTAG 120
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180
 50 TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240
 AGCATGGTGA CATGTGG 257

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60
 TATTGATAAC ATTGAAGTGA ATATANAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA 240
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240
 TACCACnGn T 251

(2) INFORMATION FOR SEQ ID NO: 4505:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGA²CTTG²TAA TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC 240
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCAATTA GGTGCAACAT 240
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAATCGG CTGTGGGTAT 300
TTTGGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120
GCTGTTAATT TACCATCACG TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180
GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

5 CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA 60
 TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180
 10 TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACTTGTA CTTCTTGATG TGCTTTGTGA 240
 ATCGGATTTC GCTCGTGCT GGTACTnG 268

(2) INFORMATION FOR SEQ ID NO: 4509:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

25 CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60
 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCACGCTT 120
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180
 30 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGCGGCTT nCACATCACA CTTAnA 296

(2) INFORMATION FOR SEQ ID NO: 4510:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

45 TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60
 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120
 GGCTTATTTC CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA 180
 50 TGTGCTGCA CCATTACCCA CTTnTTCAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240
 TAATTAAATG GTCCTGA 257

(2) INFORMATION FOR SEQ ID NO: 4511:

55

(A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

10 AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAGTATCT 60
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTAAAT CATCCATAGC AATTCTCGTT 180
 15 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240
 TGATAAATGC 250

20

(2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

30 AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT 120
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180
 35 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240
 CTCTCCCCAG CTG 253

40

(2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

50 GnCGACCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60
 nAAGTTACGT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTC AGTGTTCTTT 120
 55 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

(2) INFORMATION FOR SEQ ID NO: 4514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

| | |
|-------------------------------------------------------------------|-----|
| GTCATTGAAT ATGGAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG | 60 |
| ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCGC | 120 |
| TCTTGCAGAA CAGTTAAAAG ACCATTTTAC TGTTGTAGCC GTTGATCGTC GTGATTATGG | 180 |
| AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCGTGACA GTGATTATCG | 240 |
| TGTC | 244 |

(2) INFORMATION FOR SEQ ID NO: 4515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

| | |
|---------------------------------------------------------------------|-----|
| TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT | 60 |
| TCGAGTCGTT GATTTACACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC | 120 |
| CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA | 180 |
| AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC | 240 |
| CCA | 243 |

(2) INFORMATION FOR SEQ ID NO: 4516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180
 5 CCGTCCACCG ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240
 CCCTAACCT GAGGCCGCAA nnGTAGG 267

(2) INFORMATION FOR SEQ ID NO: 4517:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60
 AGAGCCGAAG AGAGGAAAGA AGCAACCGAT TGTCACAAGT CAAGAAAGGT CTTAGCGAC 120
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAT 240
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300
 GAACGAGAAA GAGCGCACG 319

(2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180
 CATGTCAAnG TACCATTTGC AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240
 ACATGAAAAA CGGGGAACA 259

(2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATAGGGTGTG GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC | 60 |
| 10 | CCTTGCTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA | 120 |
| | AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG | 180 |
| | TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG | 240 |
| 15 | TTTGGACGAG GGG | 253 |

(2) INFORMATION FOR SEQ ID NO: 4520:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| 20 | (A) LENGTH: 245 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

| | | |
|----|-------------------------------------------------------------------|-----|
| | AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT | 60 |
| 30 | TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT | 120 |
| | CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGChACC ATCGTCGCTA | 180 |
| | AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA | 240 |
| 35 | CTCAT | 245 |

(2) INFORMATION FOR SEQ ID NO: 4521:

| | |
|----|-------------------------------|
| | (i) SEQUENCE CHARACTERISTICS: |
| 40 | (A) LENGTH: 251 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

| | | |
|----|---------------------------------------------------------------------|-----|
| | GGGCCTAAGT GGA CTCGAAC CACCGACCTC ACGCTTATCA GGC GTGCGCT CTAACCAGCT | 60 |
| 50 | GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG | 120 |
| | TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG | 180 |
| | CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT | 240 |

55

(2) INFORMATION FOR SEQ ID NO: 4522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60
CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 120
GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG 180
TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240
ACGTTTGAA 249

(2) INFORMATION FOR SEQ ID NO: 4523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60
GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAng CATAGCTGGG TAGCTATGTG 120
TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180
CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240
GACAGTGG 248

(2) INFORMATION FOR SEQ ID NO: 4524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGAnCGGCT GTGGCTCGnA 180
 CCAATACGGG TCGGACCTGC TTrnAACCATTT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

(2) INFORMATION FOR SEQ ID NO: 4525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60
 20 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180
 25 GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240
 CGCAGTTnGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300
 C 301

(2) INFORMATION FOR SEQ ID NO: 4526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60
 40 TTTCAGTAAC TTGTnCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120
 45 CACCCATCCG CTGTAACCTC AGAGTGTCAT TGGCATTAT TACACTATCT CCAACTCCTA 180
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

| | | |
|----|-------------------------------------------------------------------|-----|
| | CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG | 60 |
| 10 | TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC | 120 |
| | ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT | 180 |
| | TCGCAACCAT nCAATCATCT GGCAGTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA | 240 |
| 15 | GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA | 300 |
| | ATACCACCCA ACACCT | 316 |

(2) INFORMATION FOR SEQ ID NO: 4528:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

| | | |
|----|-------------------------------------------------------------------|-----|
| 30 | GTCCCAAGGG TTGGGCTGTT CGCCCATTAAGCGGTACCG ACGACTGGGT TCAGAACGTC | 60 |
| | GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG | 120 |
| | TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG | 180 |
| 35 | CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC | 240 |
| | AAGATGAGAT T | 251 |

(2) INFORMATION FOR SEQ ID NO: 4529:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

| | | |
|----|-------------------------------------------------------------------|-----|
| 50 | AGTACGTGAC GTTCACTACT CTCACTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG | 60 |
| | ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT | 120 |
| | TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA | 180 |

55

ATGGTCGTTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300
 GTGACGCGAC AGTGTcNA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60
 GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120
 20 GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180
 CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60
 35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG 120
 TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180
 40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GCnCAGCCTT AACGAGTACC 240
 GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

55

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTTCATT 60
 40 GAGCAGAAAG AAAATTATGG CACCAAACCTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT GTCGTCCAC CCAACTTGG 180
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

5 GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60
 GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240
 10 AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60
 25 AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACTAC 120
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

40 TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC 180
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGThAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240
 TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60
 TATTGCGTTT GGnCTGTCTG GCCAGTGCAA GATTTC AAC GATAATTTCT AGGCGTCACT 120
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240
 50 AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

55

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 15 G_nAGTGTTCCT TTCGAACATA GCGGATTAT_n TCTTATGAAT TCAAGCTTAT TTAA_nACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCA_n TTAGCTAATA TGCAAGCACA 60
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GCGGAGG_nTG ATGAATGCCT TACGTTTGCG 120
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180
 G_nATGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCT_n CCAGCTGAG 239

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTATTAA TCGTTTAAAT TCAGTTAGTA 120
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAnATA TTATAGAAAA CATCAAAGGA 180
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTC TAnTTTTTCA TGTGCTTCCG 120
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180
 GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180
 AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA 60
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCGTTT 300
 GGCACG 306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120
 ATAAAGATTC AATTAACGCA TCAGTATTAG GATTCACTCT AATACGATTA ATAGTTTTAT 180
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTCGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180
 AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT 240
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTh CCCTCCCTCA 180
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360
 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400
 50

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

| | | |
|----|-------------------------------------------------------------------|-----|
| | ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG | 60 |
| 10 | CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTACTTCTTA AACGATTAGA | 120 |
| | AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGCG AGAAACTGGG AATACCATTG | 180 |
| | AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC | 240 |
| 15 | ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTG GATTTCATT TTGGAATGTG | 300 |
| | CGTGCAGCTT TT | 312 |

(2) INFORMATION FOR SEQ ID NO: 4553:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

| | | |
|----|-------------------------------------------------------------------|-----|
| 30 | AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAATA CCAATACCAA ACCATAGAAC | 60 |
| | AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTGAT | 120 |
| | AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA | 180 |
| 35 | TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAATAATT GCTAAATGTG GnGAATTTCT | 240 |
| | CCAGTAACAA TGGA | 254 |

(2) INFORMATION FOR SEQ ID NO: 4554:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

| | | |
|----|-------------------------------------------------------------------|-----|
| 50 | GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCn | 60 |
| | AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC | 120 |
| | TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC | 180 |

55

CTGGGGCTTG G

251

(2) INFORMATION FOR SEQ ID NO: 4555:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

15

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60
 ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCGA ATGATTTAAG 120
 AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180
 CTATCTGAAA AAGCCCTACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240
 AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

35

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG 60
 GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120
 TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180
 TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240
 ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

55

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT TTAAAATAAT TTAACATCATT 120
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180
 ACGTGTTTGA TCACCCAATT TAATGATTTC ACGCTTGTGC AATAATnATT TTCGAGACGA 240
 25 GAGGATCGGA TTAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAANTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAACT 180
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCAGATT CCGACGGAAT TTCACGTGCT 180
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240
 CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60
 GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120
 TTAGCTCCGA TTGAAACGAT GTCTTGTTTT ACAGGACTAA CAGCCATTTC AGTTTGACCA 180
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60
 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTA 120
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180
 nGACTCTGCT TTAAAATAAT TTAACTCATT GTCTGCTAAA CGTTT 225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60
 ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120
 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180
 AATTATTTCA GGTTCCTTTC TTTTGCAATT GGGTGCTTTA ACCATATCTT nTT 233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180
 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120
 TGGAGAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC 180
 TGAGCTAATT CTCCGATTTA AACTGGCCT GGGCAACGTT CTACTCTAGC GGGA ACT 237

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAAC ACAGCTCATA ATATCAAAAA 180
 GGTGCAGAGG AAATGGTTGA nngGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240
 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGA ACTAG TAATAAGTAT GTCAGTTTAA 300

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC 120
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180
 TCCAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240
 AAACATTCCA 250

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTC AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60
 10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120
 AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180
 TCAGATTCTG ACCCAGGTTC AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

25

AATCTATTTC TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60
 TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTC GATTCGTGAT 120
 30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180
 CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60
 45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120
 CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180
 50 GGCAGCAGTA GGGAATTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240
 TGCTGCAGGT TCTTCGGATC GTAAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

55

- (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTACTIONACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG 60
 ACTATAGCAA GgnGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60
 30 TTCGGTGCA n TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CnAGAGGGG AATTGCTTGA TCAACACAAG 180
 GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG 230

35 (2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

45 TCACATATCG ATAACATGAC ATAACATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT 60
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120
 50 TAGTGCCAAG GCATCCACCG TCGCCCTTA ATAACCTAAT CnATGTTTCC ACCATTTTTA 180
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

55

(A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCAATTGGAA ATACCTTACT GCCnGTTTTT 240
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30

TGATTCTAGG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60
 ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAA TAATGGTGGG CCTAAGTGGA 120
 35 CTCGAACCAC CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

(2) INFORMATION FOR SEQ ID NO: 4577:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60
 TGGGTAAAAA TnTATTAATT GGGTGGTTCG TGAAATGCAA TCTTTTAAAC GACTTCAGGG 120
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

55

(2) INFORMATION FOR SEQ ID NO: 4578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT 60
 AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC 120
 CAAAATCTTC AAACCACGAT TTACTTTGn C TACTAATTC TTTTGTAGCA ATGAGTACGC 180
 GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAAACTG ACATACTTAT 240
 TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300
 CTTGATTACG CGCGCTCAAC ATTC 324

(2) INFORMATION FOR SEQ ID NO: 4579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAA CTGATTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT 60
 GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG 120
 GTATGCATAT CGTTTAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAAT 180
 TCGTCATATT TCCAATTTTG AGTGnAAAA ATGTCACTTT TAACTTTC 229

(2) INFORMATION FOR SEQ ID NO: 4580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA 60

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180
 CGTAAGTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60
 CGACTACAGG ATTATTACCT TCTTTGATTTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120
 CTTTGTAACCT CCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCAnCT 180
 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180
 TAGGTCATAG GGTnAAAACn TTTTGGAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCCGG 240
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCGTA GCTTCGCAGA 60
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAAT 120
 40 CTATATTTAC TTAATTATCT AGTTTTCAAT GTACAATTnC TTTTtagTCA AGCGCTCGCA 180
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTCCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCACG TATTnAGCCG 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60
 TGAAGTGAAT AAGAAATCAA TCATTGCTC TTCTGTTAAA TCATGTGTTT TTTCTAATTT 120
 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGGTTGCAC AAATAATACC 180
 25 CATCGCAGCA TTGACTTCAT TGTGCAAGG CACnTTGAC TGCGGCAATC ATTCATATCC 240
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180
 45 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTAAACAGC CGATAGCTCT 60
 5 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180
 10 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60
 ATCnCATTTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120
 25 CCTCGGCTAA GAACCTTTCT TGAATTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120
 TTCGTCGTCC CACCCCAACT TGnCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180
 45 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTn TTAGCCGTGG 60
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60
 AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCAGCAT GAGTTATGTC ATGTTATCGA 120
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

(2) INFORMATION FOR SEQ ID NO: 4594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120
 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180
 45 TTATCGGTTC AGGTGCCACA GnaAGTGGAT TCCAGGTTAG CCAAGGGGT TAATCTGGAT 240
 TAATTTTTTTT Tn 252

(2) INFORMATION FOR SEQ ID NO: 4595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240
 GTTACCCGGG AGnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCAATTAG GATCTGCCGG TGCCGCACGT 60
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTTCAGCAA TTGCAACTAG CTCTGGTTTA 120
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180
 TnCATTTGTTT AGTTGGGTAC ATTAATGCnG TATTATCGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGCGCG GTAGGGTCAC 60
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTGCGCTAT CCTACTGnGG TCCCCCATC 240
 GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

55

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120
 TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC 219

35

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60
 CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120
 50 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

55

(A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTACA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120
 CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGCnAG 180
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180
 35 TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120
 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnc TAGTGATTAT TTACAACATG CCAAAGAATT 180

55

TATCCn

246

(2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAG GGTGTATGGA 120
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180
 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240
 TTTGATGG 248

(2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTC AGTTTCCAAT GACCCTCCAC GGTGAGCCG GGACTTnTCA CATCAGACTT 60
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTnG TTTTGTTTn 240
 TGGGTT 246

(2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180
 5 TGCAGTTATT TCAGTTTCTG CTTACGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAT 60
 20 GACCCCGTAA CTTCTGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCCAGAAG AGCCGCATGA 120
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180
 AGGGGCTGAC GCCTGCCCCG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAGG TGTTAnATTA AAGCAGTTTC TCGATCTGGT 60
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120
 GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

45 (2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATCGAATCG 60
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120
 GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTAAAC GCTTTTAAAT 180
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTChGA ATnGATTAGC 240
 C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180
 TTTCAnTTcG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGGATA AATATGGCGT GCGTTTGGCA 120
 ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180
 TGCAGTACCG TGTTTGTTGA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240
 TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360
 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCTAATG 240
 ACCGTTAAGG TnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180
 35 AGCTTTTTTC TACAGCTTTT ACAATATTnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTAAAnTTTA 60
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG 180
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60
 TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTCT 60
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120
 ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

(2) INFORMATION FOR SEQ ID NO: 4618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCAan 60
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 120
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60
 GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

(2) INFORMATION FOR SEQ ID NO: 4620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCATTT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120
 CATTTTTCTT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60
 TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180
 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC 240
 ACAGTCTCGG GCGATTGTCG AGTCCAC 267

(2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGCGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60
 TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180
 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

(2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA 60

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240
 5 AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTATTGAA ATCAATGAAA 300
 A 301

(2) INFORMATION FOR SEQ ID NO: 4624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20 CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60
 GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120
 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180
 25 TTTGAAAAAG GGGnAAATCA TAATCATtnG GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60
 40 CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180
 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240
 45 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300
 A 301

(2) INFORMATION FOR SEQ ID NO: 4626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATAACAAT TTACAAATAG 60
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120
 10 CATTAAATCCC ATTTTTCAnCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

(2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60
 25 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60
 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120
 45 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180
 TCCACCACAT GTTAAATATG CAGCAGAG 208

50 (2) INFORMATION FOR SEQ ID NO: 4629:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120
 ACACAACATA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180
 10 ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300
 CACTG 305

15 (2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAAACTAG ATAGTAAGTA 120
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60
 TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

55

(A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAATT ATTCGAACCA TTATTACAG 60
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTCTn TAGAAATTAG 120
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180
 CTAATGTGTT AAGAACTACT ACAT 204

35

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TCGGTTACGT TAGCCCGTCT GATGTAGAAG 120
 50 CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180
 AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

(2) INFORMATION FOR SEQ ID NO: 4635:

55

- (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

| | | |
|----|-------------------------------------------------------------------|-----|
| 10 | CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC | 60 |
| | GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTGT | 120 |
| | AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG | 180 |
| 15 | GCTTAAGTTG GCCATTTTTC ATATGGTC | 208 |

2) INFORMATION FOR SEQ ID NO: 4636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

| | |
|-------------------------------------------------------------------|-----|
| TTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTtagGAC ATAAAAAATA GTAGACCTTG | 60 |
| GGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA | 120 |
| GTAAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC | 180 |
| TTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG | 228 |

35

2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

45

| | |
|------------------------------------------------------------------|-----|
| ATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA | 60 |
| CTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCTT GAGAGGGTGA | 120 |
| CGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC | 180 |
| TCCGCAATT GGCgAAAGCT GTACGGGCAA CG | 212 |

50

2) INFORMATION FOR SEQ ID NO: 4638:

55

(A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60
 TTTTtaggg ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTTC GATAATTTTT 120
 CAGGAAGCAT TTAAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT 180
 15 TACATTTCTT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT 60
 GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA 180
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180
 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224
 55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTAAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120
 CGCTGAACTA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180
 ATCCTAAGTC TAGTGCGTCT GCCAA 205

(2) INFORMATION FOR SEQ ID NO: 4642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTTATGTn CCCAG 235

(2) INFORMATION FOR SEQ ID NO: 4643:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

(2) INFORMATION FOR SEQ ID NO: 4644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180
 GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAAG CGATTTTCGG 240
 TTCAGTCCAC TACTGGCAAT ATAAC TTGTA GAGCTAGGAC ATTGG 285

(2) INFORMATION FOR SEQ ID NO: 4645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60
 CGCTTGnTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120
 TACGAACGTG TTAAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180
 ATTTAGATGG TGGCTTTTGA TAAACA 206

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60
 CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTCnGA TA

222

(2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCCTCCA GCATTTGCTT AATGAATGCT TTTTCTTCGT 60
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120
 GncGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180
 CCGAAATTAA TGACAGTCCA 200

(2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60
 ACGCAGGAnG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120
 AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTAAA 180
 TAAGCTTGGA ATTCATTAAG A 201

(2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60
 ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTC AAGGATTACG 120

AAAGTCTGTG AGTAAGGCTG TATGGAAAGT GGTnAAAT

218

(2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60
 AGAAGTAAAA GCCATCAGGT GCGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120
 CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180
 ATTCnGATTA CTAATATnTA TG 202

(2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG 60
 AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC 120
 TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC 180
 CAAGGCAACG ATGCATAGCC GACCTGAGA 209

(2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60
 ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

(2) INFORMATION FOR SEQ ID NO: 4653:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

15 CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180
 20 AACCGGTACG TGATCACTCA ACnGn 205

(2) INFORMATION FOR SEQ ID NO: 4654:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60
 35 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180
 AAAGTACCAA TGATTTCCTA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240
 40 CTATTAATCC ACACGGGTTA GAnG 264

(2) INFORMATION FOR SEQ ID NO: 4655:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

55

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

5 (2) INFORMATION FOR SEQ ID NO: 4656:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60
 GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120
 20 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

35 TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC 60
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120
 CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAATA TAGATTTTAC CAAGCAAAAC 180
 40 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60
 55

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180
 AAAAn 185

5 (2) INFORMATION FOR SEQ ID NO: 4659:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60
 GGGAGTACGA CCGCAAGTGT ATAAC TCAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120
 20 GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180
 AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

35 ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTAAAGTCA 60
 CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120
 GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT 180
 40 GATAGAAATC ACTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240
 ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300
 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTTCGTT 360
 45 CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60
 5 CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180
 ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120
 25 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180
 CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240
 GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60
 TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120
 45 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAATCTA 180
 AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120
 GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCTGA ATCCTGTCTC 180
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACCTT 60
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180
 CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60
 TAGATTGTGG TTTTnTAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTTG GATTTTC 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120
 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180
 10 CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA 120
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180
 30 TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTAAAAACA GTTACAACAG ATGAnAATGG 60
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180
 TT 182

(2) INFORMATION FOR SEQ ID NO: 4670:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60
 CACCTTTTAA AGTATTACGT AATGTTGTGT TCGTTTACA TCTTACCCAA AGTGCTAATG 120
 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180
 10 ATTGG 185

(2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60
 25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180
 30 CATTGAGACC GCAAGGnTnT 200

(2) INFORMATION FOR SEQ ID NO: 4672:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60
 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTCGC CATTAAAGCG nACGnTGCTG 120
 45 GGTTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180
 TGTCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCTG TGCCACGCAT 240
 50 AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180
CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

CCCAGTCAAA CTGCCCCCCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180
AAGCTCCACG GGGTTCTTTC CGT 203

30

(2) INFORMATION FOR SEQ ID NO: 4675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120
GGATTCGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

45

50

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTA TTACCTCAAT ATGCTTGTCA 60
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120
TTACAAATTT AGTGTGCGnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180
AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAn 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTG TGGAGCGGAA GATAGGTTTA 60
CACCTATACC TCGTTCCGGA AGGAnTGTTT TAAAAGTGAA CTACTCCCGC AATATTAAAT 120
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180
AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACn 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT 60
10 CGCCAAGCCA TCTTTCTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG 120
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60
25 TTAAGTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180
30 CCC 183

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60
45 AGATGGTCCT CCCAGATTCC GACGAATTTT ACGTGTTCCG TCGTACTCAG GATCCACTCA 120
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180
TTCGTCTAAT GTCGTCCTTT GTA 203

50

(2) INFORMATION FOR SEQ ID NO: 4682:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60
 5 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180
 10 ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180
 TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60
 AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120
 45 AGCTTATTTA AAACTCTTTA TTCACTCGGT TTTGTAAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA 60
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120
 AGCGCCTGCT TThCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

(2) INFORMATION FOR SEQ ID NO: 4686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120
 nTTATTTTCA AAAAATCAAA TGCTCATTGA CAAAAGTAAA CTCCGCTTTT AATT 174

(2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

(2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180
 GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60
 GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT 120
 CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180
 CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCGCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60
 GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120
 TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAnA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60
 TTAAAGGGGG CCCAATTTTT CCCAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240
 TTAAGGGAAT TTAATAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300
 5 AAAATTAATT AAAnAACCCA TTTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTG 360
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60
 nTTTACTTAA AGTAAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180
 25 AAATAGGAAT ACATGAGTAA AACTCantGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

25 (2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTAACTT ATCTATTAAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120
 40 TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60
 TTGGGCGTAA ACGCGCGTAG GnGTTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120
 GGGTCATTGG AAACTGGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60
 TGACATACCA TATCGACTAG GTACCTTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120
 GGGCAAGGTC ATCTTGCAAA ATGGATTCTGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180
 TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG 240
 CGGACGCn 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 120
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120
GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60
AATGCCAATT AATTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA 120
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAATATA TGT 163

30

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTTG ATTGGCTGCA GTCGCGATGG 120
TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCn GTACCCGTCA GATATCCGCA 180
GCAATGCAAT GTTGTGCAAG TTT 203

45

(2) INFORMATION FOR SEQ ID NO: 4707:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCACAGA GGAGGCTCGT CCGCTCTGGG 60
 5 TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120
 TACCACCTAT AATCGTTTAA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

25 (2) INFORMATION FOR SEQ ID NO: 4709:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60
 TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

(2) INFORMATION FOR SEQ ID NO: 4711:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

15 TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60
 TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTCAG AATCTTTTTC 120
 AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

20 (2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

30 ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60
 CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120
 TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

35

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60
 CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120
 CCTGGGAGAT AGCTGGTTCT CTCCG 145

50

(2) INFORMATION FOR SEQ ID NO: 4714:

55

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120
 AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTGT TTGTAAAAGT GGCATTCTA 120
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGANT AAATCTTTTA AGGCTTATAA 60
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA 120
 CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60
 20 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120
 CTTAACCCTAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACTGTA ATGGTGTCGT 120
 40 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60
 TTAATTAGCT TAAACGCnGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120
 TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGCGCT AAGTAnATCG CATTAAACGT TTGTCTTCCG CCATTGAGC 60
 CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120
 TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACCTTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60
 GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120
 AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACCGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCC CTCAAGATGA nATTTCCCAA 60
 CTTGCGTTAT AAGATCCCTC AAAGATGATT AGGTAAATAG GTTCGAGGTG GAAGCATGGT 120
 30 GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAATA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60
 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120
 45 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180
 CAGCATGCCG GTGTTCTTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60
AACTCTATCC AAAGACATAC AGTCAATACA AACATTACG TATCTTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT 120
GTGATGCTGA CTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120
GCCCTCCCAT ACCTCGGG 138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCCG ATTTGTCTGA ATTCGTAACC 60
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
 5 AAAGTATTTC GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60
 AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCTAT CCGTCGTGGG CGTAGGAAAT 120
 TTnAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAATA TAGCTATTAC TATAAAAAC AGCAGTAAGC ATATTTCCAA 60
 ATTGCAAATT ATCCTACTGC TGTTCCTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120
 ACAAATTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCAACTTGC ACATnATTGC 60
 AAGCTGACTT TTCGTCACCTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120
 TACTTTGATT GAIGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT 60
 TTTTGTAACCT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

(A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCGTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60
 AGTTCAGGTA ACACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAaNT GAGCGGATGA 120
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15 (2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25 GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
 TGAGATTTC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120
 30 GAACATGGTG ACATGThATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40 GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

5 TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60
 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120
 TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180
 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

20 GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GCGCATTAC CAGAGTTGCA 60
 TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAATGCG TGTTACGTGA 120
 25 TCATGATACT GTCAn 135

(2) INFORMATION FOR SEQ ID NO: 4742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

35 ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

(2) INFORMATION FOR SEQ ID NO: 4743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120
 TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

5 (2) INFORMATION FOR SEQ ID NO: 4744:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60
 AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120
 20 TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAATTTG AATGAACAAA CATTCAAAAC 60
 TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120
 35 AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60
 50 GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120
 GACAnTGACT CCGATTCA 138

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACCT GCTGGTGnTT GGGGACCCCA CCAACTTGGC 60
 ACATTATTGG TAAGCTGACT TTTCGTCACCT TACTGTGTTG GGGCCCCGCC AACTTGCATT 120
 GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180
 GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60
 CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCT ATTTTCATGG TGTCAAAAAT 180
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

(A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAGAGT TTAAATAAG CTTGAATTCA 60
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTAAATCTT 120
 TTTATAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180
 TCCG 184

(2) INFORMATION FOR SEQ ID NO: 4752:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AAAGTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCA TGTTCTGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60
ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120
TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG 162

10 (2) INFORMATION FOR SEQ ID NO: 4754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTC CCTTAGTAGC GGCGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60
TTTGGGGGTT TGTAAGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120
CTTGGGAAAG ATGA 134

25 (2) INFORMATION FOR SEQ ID NO: 4755:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

30 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

AGAGTGCGTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60
ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120
40 TGAAGCATGn ATCGTAAGG 139

(2) INFORMATION FOR SEQ ID NO: 4756:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120
 ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAnGAT 120
 TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60
 GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120
 ACTGCTGTTC TCTATTTATA CCAnATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60
 ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG 120
 ATTTGCT 127

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCTCG TCGGGTTACC GAATTCAGAC AAACCTCCGnA ATGCCAATTA ATTAACTTG 60
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120
 AGTCCCAAAT ATATGTTAAT GAAAG 145

(2) INFORMATION FOR SEQ ID NO: 4761:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTAAACC CTAAAGAGCA 60
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180
 TTAACACACC AAAACAGCTC CCACCACCAC TAnATCGAnC AACACTAG 228

(2) INFORMATION FOR SEQ ID NO: 4762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC 120
 AGCAGGGTTG 130

(2) INFORMATION FOR SEQ ID NO: 4763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120
GTTCCACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120
TACTGCCA 128

30

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

40

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120
TTTCCATGTG GnaAC 135

45

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120
 5 CACAGC 126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
 GATTTTTAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60
 35 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
 TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60
 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

(2) INFORMATION FOR SEQ ID NO: 4770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
 ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120
 TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60
 GTGCCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120
 ATGTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 4772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTGGCTA 60
 ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTGGTGT 120
 GTACTT 126

(2) INFORMATION FOR SEQ ID NO: 4773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60
GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAGAn ACCTTGCGGT CTCAATGCGG 120
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60
TGCATCTTnA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAⁿCCAGAA ACTCCAACAC CGCCAACACC 120
AGAG 124

45

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

CCCGCTAGTC TCCACCATT TTTTACACGATGAACAT TGAAAACtA ATACAATATG 60
 CAACGTTAAT TCCAAAAAC GTAACATAA GTTACAAACA TTATTAGTA TTTATGAGCT 120
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG 120
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTGTAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCACTGCTC 120
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAACTATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60
 AACAAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

(2) INFORMATION FOR SEQ ID NO: 4780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120
 TCCTTTT 127

(2) INFORMATION FOR SEQ ID NO: 4781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60
 GTCTTATTTT TTAAAGTAT TTAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120
 CGAGACTCC 129

(2) INFORMATION FOR SEQ ID NO: 4782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTAT GTTTGnTTTG 120
 GTCAGATTTA GGACCA 136

(2) INFORMATION FOR SEQ ID NO: 4783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60
10 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60
25 nATCCCATTG CATCCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60
40 ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTCTAAAC CCGnCACAC TTTATCGTGG TGGGGAGACA GTGTTGAGC GGGCCAGTTT 60
55

AATCATTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTTAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AaATACCTTT 60
 TTCATCTTGG TCTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnc ATCATCTTTG AGGGATCTTA TAACCGCAGT 60
 TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120
 GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120
 GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG 60
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60
TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60
AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

55

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120
n CCTGATAAC 130

5 (2) INFORMATION FOR SEQ ID NO: 4794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

20 (2) INFORMATION FOR SEQ ID NO: 4795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

ntTAAAAAAA ATTCCCAATT TTTTTTGGGG GGTTGGGAAT TTAAAAATTT GGTTTTTAAC 60
CCAAAGGCCC TTTTCCCAA AATTTAAT CCCTTAAAAA TTAAAAATTT GGGAATTTTT 120
35 TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTTAATT TAACCCTTAA 180
AACCCCAAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

40 (2) INFORMATION FOR SEQ ID NO: 4796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

50 TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCgTCGAT GTGAACTCTT GGGGGCAGAT 120

55 (2) INFORMATION FOR SEQ ID NO: 4797:

(A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

25 CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

40 CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

55

TCAGTGGAT GATTCGTGAA ATTGAAACGC AAGATTTCGA TATCGAnCAC CT

112

(2) INFORMATION FOR SEQ ID NO: 4801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60

ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCACC GTGAGTGCTT 60

TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAAATT AACGTCTTCT GCAGTCGCAC 120

CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180

CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60

AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60
GTTAGGGGTT TCCGCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

10

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60
CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCCGAT 108

25

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60
GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

40

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60
TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

55

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60
 ATCATTGCTA GCTTTTCTTG TATTAAGTGA TATTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTTGA TTGGAATTTTC 60
 TCCATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120
 TACCTGACTT CAACTGACCA GGGTAGACAC 150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGCCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60
 AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCG AGGAAGACAC 60
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120
 ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60
 35 TAGCCCTAAA GCTATTTCCG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

(A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GGCGGCGGTT GAACCCGTCA TTCTGCACCA 60
 TTTATTCTTA CATATTGCCG G_nCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT 120
 AGGTT 125

15 (2) INFORMATION FOR SEQ ID NO: 4816:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

25 GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60
 CTGTTGCTTA CACTGAAGAC GTTTATG_nTT TCTGGCGTCC AACT 104

30 (2) INFORMATION FOR SEQ ID NO: 4817:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40 GTCGGGTAAG TTCCGGCCCC CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACG_nGAG 60
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45 (2) INFORMATION FOR SEQ ID NO: 4818:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

55

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120

A 121

5 (2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

15 TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

20 (2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

30 CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

35 (2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

45 TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

50 (2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

25 TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60

CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA ACTAGAGn 108

40

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120
 ATCCTTGTAT TCGGTGTCAT AaAGTCTTTG CTCCTTGAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60
 AAAGAAAATG GTTGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60
 TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCACGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60
 GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

5 (2) INFORMATION FOR SEQ ID NO: 4830:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
 TTTCGTTTCAG TCAACTACTG CCAATATAAC TTTGTAGAGC ATTGA 105

20 (2) INFORMATION FOR SEQ ID NO: 4831:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60
 AGGTGCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

35 (2) INFORMATION FOR SEQ ID NO: 4832:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

45 TnTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60
 TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

50 (2) INFORMATION FOR SEQ ID NO: 4833:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60
CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120
TTTTCAGCAT CAATTTGATC AATC 144

10 (2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

(2) INFORMATION FOR SEQ ID NO: 4835:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60
CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG 60
TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60
 CGGAATTTCA ATTTGCAnGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60
 GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60
 ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTTGGCTTT 120
 5 CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTIONAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60
 20 CATTCACTCA ACTACTGCCA ATATAATATT GnaAACTATA GGACATTTAT TAGTGTTTCA 120
 GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAAGna GGAACATGTG TGTAAGTAGC 60
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

GA CTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTGGAAC GCACGTGnCC CTGCCCATAC 60
 CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120
 CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA CTTACCG 60
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60
 TTATAGTTAC GGTCCGCCGT TTA CTTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120
 CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTGG TGGGAGAACC 60
TAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60
GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

30 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTnTA 60
35 ATCGATGGGG GACCCATAGG ATAGCGAACC TCGGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

45 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60
50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

55

- (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
 CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
 25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120
 CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60
 TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCCTG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAAGTCGCC GGTTCACTCT ACAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60

CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCT CTCCTCTTT CCGGGGTnGC 120

TTTTTCAACC TTTTCCCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60

CTCTCGTTAA GGAAGTCGGC AACTGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60

AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120
 GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
 TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
CGGTTTAGCA GAGACCTGTG TTTTGTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

ACGAACGAT TGTCTTGCCT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
CTACTGCTC ATCAGGGATT ACAAACC 87

2) INFORMATION FOR SEQ ID NO: 4869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120
 AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

(2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTnAACC 60
 AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

(2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCAGTG CGGCTCTTCT 60
 GGGCGTTAAC CCTAAAGAGC ACCC 84

(2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60
 ATGATTTCAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60
GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

15 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTCG ATCCCGCTAG TCTCCACCAT 60
20 TATTTGTACA TTGAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

30 TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60
35 CGAACTGAAT AAATAAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

45 AACGCGTTAA ATCTTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

(A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60
 CGGGGAGGTT TGNCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60
 CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60
 AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60
 CTTACGCTT CTTCGCATT 80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCACGG CTCAACCGTG GAGGGTCATT GGAACTGGA AAATTGAGT 60
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120
 CGGTAA 127

(2) INFORMATION FOR SEQ ID NO: 4884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTGT GAGACCTCTA TTCTACCTTG AACTATGCCC 60
 5 CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
 20 GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60
 35 TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAATGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60
 50 ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGTCCGA 60

GTTCCTTAAC GAGAGT 76

25

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG GCAGTTCGAA 60
TCTGCCCCC TCCATTTATT ATTTTAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120
 TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTTCGGATTT AATTTGATTC ATTTGTTGCG TAATTTTCTA AGCCATTTTA TGAAAAGAGT 60
 GATTTAATTC ATAAATTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
 AAACCAATTA GTA 73

35 (2) INFORMATION FOR SEQ ID NO: 4898:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
 TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60
 TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60
 CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60
 AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60
 CAAAACTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60
AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
TCCTCTTCTT GGCTCTGCTT CTATTGCGCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

30 (2) INFORMATION FOR SEQ ID NO: 4905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGA CT TGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60
TTATCGTGGT GGGGA 75

45 (2) INFORMATION FOR SEQ ID NO: 4906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGACTCAGAT CAGATAGTGn CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA
 AGGTTTACCA

60

70

(2) INFORMATION FOR SEQ ID NO: 4908:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTC GGTGGGACAC AATAGTGTTG
 ACTTTGAAGA AGATACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC
 C

60

120

121

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG
 TTAAGTCCCG

60

70

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

GGACACCCGG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
 TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60
 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTGAT 120
 GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60
 AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGT 69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC 60
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

5 (2) INFORMATION FOR SEQ ID NO: 4918:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60
ACATATGT 68

20 (2) INFORMATION FOR SEQ ID NO: 4919:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
AGTGACAATA CTTTCAGGG 78

35 (2) INFORMATION FOR SEQ ID NO: 4920:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTTCGATTCTG 60
TACTTCGC 68

50 (2) INFORMATION FOR SEQ ID NO: 4921:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60
20 GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60
35 TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTATTT TTTACACGAT GACATGAAAC 60
50 TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTTG GGCAGTATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
GTGGGTCCCC ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGCTAGAG CACTTGGTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60
ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60
 CACCAGTGGG CGA 73

5

(2) INFORMATION FOR SEQ ID NO: 4933:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60
 GTCTG 65

20

(2) INFORMATION FOR SEQ ID NO: 4934:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60
 TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

35

(2) INFORMATION FOR SEQ ID NO: 4935:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60
 GGATAACGGT TG 72

50

(2) INFORMATION FOR SEQ ID NO: 4936:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

15 ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60
20 TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

30 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
35 GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

45 TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60
50 CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60
 TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60
 CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60
 TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

55

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
 GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60
 CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60
 TCCCTATAGC GCGGACGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
 TACAGCGCTG AACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTCC 60

5

T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60

20

TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60

35

CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 78 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60

50

TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGCGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGCGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

50

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTGGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

20

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAATCTAT ATTTTACTTA CTTATCTAGT 60

35

TTTCAATGTA CAATTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG

59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA

59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA

59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA

59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGAATGCCGG TGACAAACCG

60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTGA AGAAACAATC TCAAATAAAG AATTGTTTG

59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG

59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG

59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT

60

(2) INFORMATION FOR SEQ ID NO: 4968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTtagagg CGACGCCcag TCAAactgcc CGCTGACact GTCTCCCacc 60

(2) INFORMATION FOR SEQ ID NO: 4969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTact GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTCACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60

15

AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATCATGC ATAAGAAATA CTAATTTTC 58

30

(2) INFORMATION FOR SEQ ID NO: 4974:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

40

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

55

(2) INFORMATION FOR SEQ ID NO: 4976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTCGA CCCTGACTCG ACTTG TAGGT CTCGCAGTCA AGCTCCCTT

59

(2) INFORMATION FOR SEQ ID NO: 4977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT

58

(2) INFORMATION FOR SEQ ID NO: 4978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG

58

(2) INFORMATION FOR SEQ ID NO: 4979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC

60

(2) INFORMATION FOR SEQ ID NO: 4980:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

AAGATGAATC AAAGT 75

25

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

10 (2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

20

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

35

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC 60

50

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

10

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

20

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG 57

35

(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

45

CAAACCTCTCG TGGTGTGACG GCGGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC 60

ATGCCCGTCT ACG 73

50

(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60

TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

50 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCACTAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60

AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTC AGTCAACTAC TGCCAATATA ACTTCGT 57

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

56

(2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC

60

TTGGG

65

(2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

56

(2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGTATAA ACAGTCGCTT

60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCAGT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60
GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

40

(2) INFORMATION FOR SEQ ID NO: 5016:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

(2) INFORMATION FOR SEQ ID NO: 5017:

55

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

35 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

(2) INFORMATION FOR SEQ ID NO: 5020:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTTTGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

35

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT 60
5 CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60
20 AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

35 (2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

45 GGGCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTCTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTCTG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTIONACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 5036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAAGTTCTG TGTTCCGGCAT GGGAACAGGT GTGA

54

(2) INFORMATION FOR SEQ ID NO: 5037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG

56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

25 (2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35 TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

40 (2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

3GCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

50

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

10

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

35

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

50

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

5 CGTCATCCCC ACCTTCCTCC GGTTTGTAC CCGCAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

30 CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA 53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT 59

45 (2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAAGAC GTACTTCATG 60
TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

30

(2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

55

(2) INFORMATION FOR SEQ ID NO: 5055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG

53

(2) INFORMATION FOR SEQ ID NO: 5056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA
CAA

60

63

(2) INFORMATION FOR SEQ ID NO: 5057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC

54

(2) INFORMATION FOR SEQ ID NO: 5058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG

53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

(2) INFORMATION FOR SEQ ID NO: 5060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT

(2) INFORMATION FOR SEQ ID NO: 5061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

(2) INFORMATION FOR SEQ ID NO: 5062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA

(2) INFORMATION FOR SEQ ID NO: 5063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTGAC GTTT TAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAACT

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTAAAG AGTGCGTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGTTGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

(2) INFORMATION FOR SEQ ID NO: 5081:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

(2) INFORMATION FOR SEQ ID NO: 5082:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTTCTTA

CG

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10 GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC 60

CCGAGGAGCG GATTAACA 78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50 AAGTTGTTCT CAGTTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T

51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC C

51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA

55

5

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

15

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

30

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

40

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

45

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60
CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA 50

(2) INFORMATION FOR SEQ ID NO: 5107:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT 50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTA CTTTTTA TTTTGACGTT TTAGACATAA 50

(2) INFORMATION FOR SEQ ID NO: 5109:

50

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCCGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACITTTAC TTACTATCTA

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGCTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

T

(2) INFORMATION FOR SEQ ID NO: 5122:

(A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

TAGCGACTCA GATTCAGACA GCGATTCAGA CAGCGACTCA GACTCAGATA

50

10

1

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT

50

1

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

TACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT

60

35

C

2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

.GAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT

60

A

.GAA

64

50

A

2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG

50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTTCGTTCAA TTTATG GGG CCATTTATGG

50

35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

(2) INFORMATION FOR SEQ ID NO: 5135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

(2) INFORMATION FOR SEQ ID NO: 5136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

(2) INFORMATION FOR SEQ ID NO: 5138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

(2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT 56

25 (2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35 AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

50 (2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAC AATTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT 60
 5 CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GAAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAAC TT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60
ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60
TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

(2) INFORMATION FOR SEQ ID NO: 5157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G 51

(2) INFORMATION FOR SEQ ID NO: 5158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

(2) INFORMATION FOR SEQ ID NO: 5159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

(2) INFORMATION FOR SEQ ID NO: 5160:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT 60
T 61

2) INFORMATION FOR SEQ ID NO: 5161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

3ACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51 25 A

2) INFORMATION FOR SEQ ID NO: 5162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55 C

2) INFORMATION FOR SEQ ID NO: 5163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

TTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAACG TCTATGACGT 60 50 C

GTAGTATAA GATTCCGTGT A 81 C

2) INFORMATION FOR SEQ ID NO: 5164:

40

45

55

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60
AA 62

40

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

55

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTGTACA TTGAACTAG ATAAGTAGTA AATATA 56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA 55

(2) INFORMATION FOR SEQ ID NO: 5170:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA 52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAAGCT GATTCTATT 50

50

(2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

5 AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

30 CAACTCTCGT TAAGGAACTC GGCAAATAC CCCGTAAGTT CGGAGTAGGT CTCTTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCTG CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACCTT ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

15

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC

60

GCAATAT

67

(2) INFORMATION FOR SEQ ID NO: 5182:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

30

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAGTAG CGAAGGCAAC TTTCT

55

(2) INFORMATION FOR SEQ ID NO: 5183:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

50

(2) INFORMATION FOR SEQ ID NO: 5184:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

55

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

15

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

55

(2) INFORMATION FOR SEQ ID NO: 5186:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

50

30

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

40

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

50

(2) INFORMATION FOR SEQ ID NO: 5188:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

50

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGTAC CCTTGGACCG ACTACAGCCC AGATCGATGA

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1 5 10 15

EP 0 786 519 A2

| | 20 | 25 | 30 |
|----|------------------------------------------------------------------------------------|----|----|
| 5 | Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45 | | |
| | Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60 | | |
| 10 | Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80 | | |
| | Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95 | | |
| 15 | Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110 | | |
| | Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125 | | |
| 20 | Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140 | | |
| | Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160 | | |
| 25 | Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175 | | |
| | Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190 | | |
| 30 | Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205 | | |
| | Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220 | | |
| 35 | Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240 | | |
| 40 | Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255 | | |
| | Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270 | | |
| 45 | Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285 | | |
| | Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300 | | |
| 50 | Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320 | | |

55

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Val | Ile | Lys | Met | Leu | Val | Val | Thr | Leu | Ala | Phe | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Leu | Ala | Gly | Cys | Ser | Gly | Asn | Ser | Asn | Lys | Gln | Ser | Ser | Asp | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Asp | Lys | Glu | Thr | Thr | Ser | Ile | Lys | His | Ala | Met | Gly | Thr | Thr | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Lys | Gly | Lys | Pro | Lys | Arg | Val | Val | Thr | Leu | Tyr | Gln | Gly | Ala | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asp | Val | Ala | Val | Ser | Leu | Gly | Val | Lys | Pro | Val | Gly | Ala | Val | Glu | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Trp | Thr | Gln | Lys | Pro | Lys | Phe | Glu | Tyr | Ile | Lys | Asn | Asp | Leu | Lys | Asp |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Thr | Lys | Ile | Val | Gly | Gln | Glu | Pro | Ala | Pro | Asn | Leu | Glu | Glu | Ile | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Lys | Leu | Lys | Pro | Asp | Leu | Ile | Val | Ala | Ser | Lys | Val | Arg | Asn | Glu | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Tyr | Asp | Gln | Leu | Ser | Lys | Ile | Ala | Pro | Thr | Val | Ser | Thr | Asp | Thr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Phe | Lys | Phe | Lys | Asp | Thr | Thr | Lys | Leu | Met | Gly | Lys | Ala | Leu | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Lys | Glu | Lys | Glu | Ala | Glu | Asp | Leu | Leu | Lys | Lys | Tyr | Asp | Asp | Lys | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Ala | Phe | Gln | Lys | Asp | Ala | Lys | Ala | Lys | Tyr | Lys | Asp | Ala | Trp | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Lys | Ala | Ser | Val | Val | Asn | Phe | Arg | Ala | Asp | His | Thr | Arg | Ile | Tyr |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ala | Gly | Gly | Tyr | Ala | Gly | Glu | Ile | Leu | Asn | Asp | Leu | Gly | Phe | Lys | Arg |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asn | Lys | Asp | Leu | Gln | Lys | Gln | Val | Asp | Asn | Gly | Lys | Asp | Ile | Ile | Gln |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Leu | Thr | Ser | Lys | Glu | Ser | Ile | Pro | Leu | Met | Asn | Ala | Asp | His | Ile | Phe |
| | | | | 245 | | | | | 250 | | | | | 255 | |

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
260 265 270

5 Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
290 295 300

10 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
325 330

15

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

30 Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
20 25 30

35

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
50 55 60

40

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
85 90 95

45

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
100 105 110

50

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
130 135 140

55

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
145 150 155 160

EP 0 786 519 A2

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
165 170 175

5 Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
195 200 205

10 Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
210 215 220

Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
225 230 235 240

15 Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
245 250 255

Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
260 265 270

20 Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
275 280 285

Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
290 295 300

25 Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
1 5 10 15

45 Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
20 25 30

Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
35 40 45

Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
50 55 60

55 Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
65 70 75 80

Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
195 200 205

Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
210 215 220

25 Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
20 25 30

EP 0 786 519 A2

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
35 40 45

Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
5 50 55 60

Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
65 70 75 80

Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
10 85 90 95

Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
100 105 110

Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
15 115 120 125

Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
20 130 135 140

Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
145 150 155 160

Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
25 165 170 175

Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
180 185 190

Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
30 195 200 205

Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
210 215 220

Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
35 225 230 235 240

Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
245 250 255

Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
40 260 265 270

Lys

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

| | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5 | Met | Lys | Lys | Ile | Lys | Tyr | Ile | Leu | Val | Val | Phe | Val | Leu | Ser | Leu | Thr | 1 | 5 | 10 | 15 |
| | Val | Leu | Ser | Gly | Cys | Ser | Leu | Pro | Gly | Leu | Gly | Ser | Lys | Ser | Thr | Lys | 20 | 25 | 30 | |
| 10 | Asn | Asp | Val | Lys | Ile | Thr | Ala | Leu | Ser | Thr | Ser | Glu | Ser | Gln | Ile | Ile | 35 | 40 | 45 | |
| | Ser | His | Met | Leu | Arg | Leu | Leu | Ile | Glu | His | Asp | Thr | His | Gly | Lys | Ile | 50 | 55 | 60 | |
| 15 | Lys | Pro | Thr | Leu | Val | Asn | Asn | Leu | Gly | Ser | Ser | Thr | Ile | Gln | His | Asn | 65 | 70 | 75 | 80 |
| | Ala | Leu | Ile | Asn | Gly | Asp | Ala | Asn | Ile | Ser | Gly | Val | Arg | Tyr | Asn | Gly | 85 | 90 | 95 | |
| 20 | Thr | Asp | Leu | Thr | Gly | Ala | Leu | Lys | Glu | Ala | Pro | Ile | Lys | Asn | Pro | Lys | 100 | 105 | 110 | |
| | Lys | Ala | Met | Ile | Ala | Thr | Gln | Gln | Gly | Phe | Lys | Lys | Lys | Phe | Asp | Gln | 115 | 120 | 125 | |
| 25 | Thr | Phe | Phe | Asp | Ser | Tyr | Gly | Phe | Ala | Asn | Thr | Tyr | Ala | Phe | Met | Val | 130 | 135 | 140 | |
| | Thr | Lys | Glu | Thr | Ala | Lys | Lys | Tyr | His | Leu | Glu | Thr | Val | Ser | Asp | Leu | 145 | 150 | 155 | 160 |
| 30 | Ala | Lys | His | Ser | Lys | Asp | Leu | Arg | Leu | Gly | Met | Asp | Ser | Ser | Trp | Met | 165 | 170 | 175 | |
| | Asn | Arg | Lys | Gly | Asp | Gly | Tyr | Glu | Gly | Phe | Lys | Lys | Glu | Tyr | Gly | Phe | 180 | 185 | 190 | |
| 35 | Asp | Phe | Gly | Thr | Val | Arg | Pro | Met | Gln | Ile | Gly | Leu | Val | Tyr | Asp | Ala | 195 | 200 | 205 | |
| 40 | Leu | Asn | Ser | Glu | Lys | Leu | Asp | Val | Ala | Leu | Gly | Tyr | Ser | Thr | Asp | Gly | 210 | 215 | 220 | |
| | Arg | Ile | Ala | Ala | Tyr | Asp | Leu | Lys | Val | Leu | Lys | Asp | Asp | Lys | Gln | Phe | 225 | 230 | 235 | 240 |
| 45 | Phe | Pro | Pro | Tyr | Ala | Ala | Ser | Ala | Val | Ala | Thr | Asn | Glu | Leu | Leu | Arg | 245 | 250 | 255 | |
| | Gln | His | Pro | Glu | Leu | Lys | Thr | Thr | Ile | Asn | Lys | Leu | Thr | Gly | Lys | Ile | 260 | 265 | 270 | |
| 50 | Ser | Thr | Ser | Glu | Met | Gln | Arg | Leu | Asn | Tyr | Glu | Ala | Asp | Gly | Lys | Gly | 275 | 280 | 285 | |
| | Lys | Glu | Pro | Ala | Val | Val | Ala | Glu | Glu | Phe | Leu | Lys | Lys | His | His | Tyr | 290 | 295 | 300 | |

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Leu | Thr | Thr | Leu | Leu | Leu | Ala | Ser | Thr | Leu | Leu | Ile | Ala | 1 | 5 | 10 | 15 |
| Ala | Cys | Gly | Asn | Asp | Asp | Ser | Lys | Lys | Asp | Asp | Ser | Lys | Thr | Ser | Lys | 20 | 25 | 30 | |
| Lys | Asp | Asp | Gly | Val | Lys | Ala | Glu | Leu | Lys | Gln | Ala | Thr | Lys | Ala | Tyr | 35 | 40 | 45 | |
| Asp | Lys | Tyr | Thr | Asp | Glu | Gln | Leu | Asn | Glu | Phe | Leu | Lys | Gly | Thr | Glu | 50 | 55 | 60 | |
| Lys | Phe | Val | Lys | Ala | Ile | Glu | Asn | Asn | Asp | Met | Ala | Gln | Ala | Lys | Ala | 65 | 70 | 75 | 80 |
| Leu | Tyr | Pro | Lys | Val | Arg | Met | Tyr | Tyr | Glu | Arg | Ser | Glu | Pro | Val | Ala | 85 | 90 | 95 | |
| Glu | Ala | Phe | Gly | Asp | Leu | Asp | Pro | Lys | Ile | Asp | Ala | Arg | Leu | Ala | Asp | 100 | 105 | 110 | |
| Met | Lys | Glu | Glu | Lys | Lys | Glu | Lys | Glu | Trp | Ser | Gly | Tyr | His | Lys | Ile | 115 | 120 | 125 | |
| Glu | Lys | Ala | Leu | Tyr | Glu | Asp | Lys | Lys | Ile | Asp | Asp | Val | Thr | Lys | Lys | 130 | 135 | 140 | |
| Asp | Ala | Gln | Gln | Leu | Leu | Lys | Asp | Ala | Lys | Glu | Leu | His | Ala | Lys | Ala | 145 | 150 | 155 | 160 |
| Asp | Thr | Leu | Asp | Ile | Thr | Pro | Lys | Leu | Met | Leu | Gln | Gly | Ser | Val | Asp | 165 | 170 | 175 | |
| Leu | Leu | Asn | Glu | Val | Ala | Thr | Ser | Lys | Ile | Thr | Gly | Glu | Glu | Glu | Ile | 180 | 185 | 190 | |
| Tyr | Ser | His | Thr | Asp | Leu | Tyr | Asp | Phe | Lys | Ala | Asn | Val | Glu | Gly | Ala | 195 | 200 | 205 | |
| Gln | Lys | Ile | Tyr | Asp | Leu | Phe | Lys | Pro | Ile | Leu | Glu | Lys | Lys | Asp | Lys | 210 | 215 | 220 | |

EP 0 786 519 A2

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175

EP 0 786 519 A2

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
180 185 190

5 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
210 215 220

10 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

15 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
1 5 10 15

Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
20 25 30

40 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
35 40 45

Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
50 55 60

45 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
65 70 75 80

Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
85 90 95

50 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
100 105 110

Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
115 120 125

55

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
130 135 140

5 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
165 170 175

10 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
195 200 205

15

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

30 Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
1 5 10 15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
20 25 30

35 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
35 40 45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
50 55 60

40 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
65 70 75 80

45 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
85 90 95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
100 105 110

50 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
115 120 125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
130 135 140

55 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 165 170 175

Arg Ala Cys Glu Pro Asp Lys Tyr
 180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
 1 5 10 15
 Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
 20 25 30
 Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
 35 40 45
 Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
 50 55 60
 Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65 70 75 80
 Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85 90 95
 Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
 100 105 110
 Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
 115 120 125
 Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
 130 135 140
 Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
 145 150 155 160
 Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
 165 170 175
 Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
 180 185 190
 Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
 195 200 205
 Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
 210 215 220

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Asn | Val | Asp | Gly | Ile | Ala | Leu | Val | Lys | Asn | Ala | His | Pro | His | Pro |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Lys | Arg | Lys | Lys | Leu | Val | Gln | Tyr | Leu | Thr | Ser | Arg | Ser | Val | Gln | Gln |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Arg | Leu | Val | Ala | Glu | Phe | Asp | Ala | Lys | Ser | Ile | | | | | |
| | | 275 | | | | | 280 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

| | | | | | | | | | | | | | | | |
|------------|-----------|------------|------------|------------|------------|------------|-----------|------------|------------|-----------|------------|------------|------------|------------|------------|
| Met 1 | Lys | Lys | Phe | Ile 5 | Gly | Ser | Val | Leu | Ala 10 | Thr | Thr | Leu | Ile | Leu 15 | Gly |
| Gly | Cys | Ser | Thr 20 | Met | Glu | Asn | Glu | Ser | Lys | Lys | Asp | Thr | Lys 30 | Thr | Glu |
| Thr | Lys | Ser 35 | Val | Pro | Glu | Glu | Met 40 | Glu | Ala | Ser | Lys | Tyr 45 | Val | Gly | Gln |
| Gly | Phe 50 | Gln | Pro | Pro | Ala | Glu 55 | Lys | Asn | Ala | Ile | Glu 60 | Phe | Ala | Lys | Lys |
| His 65 | Arg | Lys | Glu | Phe | Glu 70 | Lys | Val | Gly | Glu | Gln 75 | Phe | Phe | Lys | Asp | Asn 80 |
| Phe | Gly | Leu | Lys | Val 85 | Lys | Ala | Thr | Asn | Val 90 | Val | Gly | Lys | Asp | Asp 95 | Gly |
| Val | Glu | Val | Tyr 100 | Val | His | Cys | Glu | Asp 105 | His | Gly | Ile | Val | Phe 110 | Asn | Ala |
| Ser | Leu | Pro 115 | Leu | Tyr | Lys | Asp | Ala | Ile 120 | His | Gln | Lys | Gly 125 | Ser | Met | Arg |
| Ser 130 | Asn | Asp | Asn | Gly | Asp | Asp 135 | Met | Ser | Met | Met | Val 140 | Gly | Thr | Val | Leu |
| Ser 145 | Gly | Phe | Glu | Tyr | Arg 150 | Ala | Gln | Lys | Glu | Lys | Tyr | Asp | Asn | Leu | Tyr 160 |
| Lys | Phe | Phe | Lys | Glu 165 | Asn | Glu | Lys | Lys | Tyr 170 | Gln | Tyr | Thr | Gly | Phe 175 | Thr |

180 185 190
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
 195 200 205
 5 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
 210 215 220
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
 225 230 235 240
 10 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
 245 250 255
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
 260 265 270
 15 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
 275 280 285
 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val
 290 295 300
 20 His Ser Lys Asp Glu
 305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
 1 5 10 15
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
 20 25 30
 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
 35 40 45
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
 50 55 60
 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
 65 70 75 80
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
 85 90 95

100 105 110
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His
 115 120 125
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp
 130 135 140
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His
 10 145 150 155 160
 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln
 165 170 175
 15 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys
 180 185 190
 Ser

20 (2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

35 Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala
 1 5 10 15
 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser
 20 25 30
 40 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe
 35 40 45
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys
 50 55 60
 45 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser
 65 70 75 80
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile
 85 90 95
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe
 100 105 110
 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn
 115 120 125
 55

EP 0 786 519 A2

| | | | | | | |
|----|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
| | 130 | | 135 | | 140 | |
| | Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala | | | | | |
| | 145 | | 150 | | 155 | 160 |
| 5 | Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu | | | | | |
| | | 165 | | 170 | | 175 |
| | Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp | | | | | |
| 10 | | 180 | | 185 | | 190 |
| | Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn | | | | | |
| | | 195 | | 200 | | 205 |
| | Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp | | | | | |
| 15 | | 210 | | 215 | | 220 |
| | Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn | | | | | |
| | 225 | | 230 | | 235 | 240 |
| | Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser | | | | | |
| 20 | | 245 | | 250 | | 255 |
| | Lys Ser Lys | | | | | |

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

| | |
|-----------------------------------------------------------------|----------|
| Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile | |
| 1 | 5 10 15 |
| Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn | |
| | 20 25 30 |
| Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln | |
| | 35 40 45 |
| Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser | |
| | 50 55 60 |
| Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly | |
| 65 | 70 75 80 |
| Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp | |
| | 85 90 95 |

100 105 110
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
 115 120 125
 5
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
 130 135 140
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys
 145 150 155 160
 10
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
 165 170 175
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
 180 185 190
 15
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
 195 200

20 (2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
 1 5 10 15
 35
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
 20 25 30
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
 35 40 45
 40
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
 50 55 60
 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
 65 70 75 80
 45
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
 85 90 95
 50
 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
 100 105 110
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
 115 120 125
 55

EP 0 786 519 A2

[illegible]

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

50 Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr
1 5 10 15
Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
20 25 30

EP 0 786 519 A2

| | 35 | 40 | 45 |
|----|---------|---------|---------|
| 5 | Asn 50 | Leu 55 | Leu 60 |
| | Tyr 65 | Lys 70 | Asn 75 |
| 10 | Ala 85 | Arg 90 | Gly 95 |
| | Ala 100 | Lys 105 | Val 110 |
| 15 | Gly 115 | His 120 | Met 125 |
| | Asn 130 | Gly 135 | His 140 |
| 20 | Arg 145 | Tyr 150 | Glu 155 |
| | Lys 165 | His 170 | Met 175 |
| 25 | Met 180 | His 185 | Tyr 190 |
| | Glu 195 | Lys 200 | Gly 205 |
| 30 | Lys 210 | Val 215 | Cys 220 |
| | Leu 225 | Asp 230 | Val 235 |
| 35 | Val 245 | Lys 250 | Arg 255 |
| | Ser 260 | His 265 | Val 270 |
| 40 | Thr 275 | Ser 280 | Thr 285 |
| | Ser 290 | Thr 295 | Gln 300 |
| 45 | Asn 305 | Asp 310 | Pro 315 |
| | Ala 320 | | |
| 50 | Ala 325 | | |

(2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Ile Met Leu Leu Val Val
 1 5 10 15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
 20 25 30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 50 55 60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
 65 70 75 80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
 85 90 95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
 100 105 110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
 115 120 125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
 130 135 140

Val Asp Tyr Trp
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
 1 5 10 15

55

20

25

30

His

5

(2) INFORMATION FOR SEQ ID NO:5212:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160

45

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
165 170 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180 185 190

50

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
195 200 205

55

EP 0 786 519 A2

| | 210 | | 215 | | 220 | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Ala | Glu | Ala | Tyr | Arg | Asn | Gly | Leu | Val | Asn | Ala | Pro | Leu | Ser | Arg | Leu | |
| | 225 | | | | | 230 | | | | 235 | | | | | | 240 | |
| 5 | Glu | Ala | Gly | Ile | Ala | His | Ser | Tyr | Val | Ser | Gly | Asn | Thr | Val | Trp | Gln | |
| | | | | 245 | | | | | | 250 | | | | | 255 | | |
| | Ala | Leu | Asp | Glu | Ser | Gln | Val | Gly | Trp | His | Thr | Ala | Asn | Gln | Ile | Gly | |
| 10 | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Asn | Lys | Tyr | Tyr | Tyr | Gly | Ile | Glu | Val | Cys | Gln | Ser | Met | Gly | Ala | Asp | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| | Asn | Ala | Thr | Phe | Leu | Lys | Asn | Glu | Gln | Ala | Thr | Phe | Gln | Glu | Cys | Ala | |
| 15 | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | Arg | Leu | Leu | Lys | Lys | Trp | Gly | Leu | Pro | Ala | Asn | Arg | Asn | Thr | Ile | Arg | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| | Leu | His | Asn | Glu | Phe | Thr | Ser | Thr | Ser | Cys | Pro | His | Arg | Ser | Ser | Val | |
| 20 | | | | 325 | | | | | | 330 | | | | | 335 | | |
| | Leu | His | Thr | Gly | Phe | Asp | Pro | Val | Thr | Arg | Gly | Leu | Leu | Pro | Glu | Asp | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| | Lys | Arg | Leu | Gln | Leu | Lys | Asp | Tyr | Phe | Ile | Lys | Gln | Ile | Arg | Ala | Tyr | |
| 25 | | | 355 | | | | | 360 | | | | | 365 | | | | |
| | Met | Asp | Gly | Lys | Ile | Pro | Val | Ala | Thr | Val | Ser | Asn | Glu | Ser | Ser | Ala | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |
| 30 | Ser | Ser | Asn | Thr | Val | Lys | Pro | Val | Ala | Ser | Ala | Trp | Lys | Arg | Asn | Lys | |
| | | | | | | 390 | | | | | 395 | | | | | 400 | |
| | Tyr | Gly | Thr | Tyr | Tyr | Met | Glu | Glu | Ser | Ala | Arg | Phe | Thr | Asn | Gly | Asn | |
| 35 | | | | 405 | | | | | | 410 | | | | | 415 | | |
| | Gln | Pro | Ile | Thr | Val | Arg | Lys | Val | Gly | Pro | Phe | Leu | Ser | Cys | Pro | Val | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | |
| | Gly | Tyr | Gln | Phe | Gln | Pro | Gly | Gly | Tyr | Cys | Asp | Tyr | Thr | Glu | Val | Met | |
| 40 | | | 435 | | | | | 440 | | | | | 445 | | | | |
| | Leu | Gln | Asp | Gly | His | Val | Trp | Val | Gly | Tyr | Thr | Trp | Glu | Gly | Gln | Arg | |
| | | | 450 | | | | 455 | | | | | 460 | | | | | |
| | Tyr | Tyr | Leu | Pro | Ile | Arg | Thr | Trp | Asn | Gly | Ser | Ala | Pro | Pro | Asn | Gln | |
| 45 | | | | | | 470 | | | | | 475 | | | | | 480 | |
| | Ile | Leu | Gly | Asp | Leu | Trp | Gly | Glu | Ile | Ser | | | | | | | |
| | | | | | 485 | | | | | 490 | | | | | | | |

50 (2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

55

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
 1 5 10 15
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
 20 25 30
 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
 35 40 45
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
 50 55 60
 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
 65 70 75 80
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
 85 90 95
 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
 100 105 110
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
 115 120 125
 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
 130 135 140
 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
 145 150 155 160
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
 165 170 175
 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
 180 185 190
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
 195 200 205
 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
 210 215 220
 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
 225 230 235 240
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
 245 250 255
 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
 290 295

5

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

20

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
 1 5 10 15

Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
 20 25 30

25

Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
 35 40 45

Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
 50 55 60

30

Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
 65 70 75 80

35

Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
 85 90 95

Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
 100 105 110

40

Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
 115 120 125

Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
 130 135 140

45

Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
 145 150 155 160

Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
 165 170 175

50

Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

55

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala
 1 5 10 15

15 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala
 20 25 30

Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp
 35 40 45

20 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu
 50 55 60

Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Asp Gly Thr Glu
 65 70 75 80

25 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr
 85 90 95

Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr
 100 105 110

30 Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly
 115 120 125

35 Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly
 130 135 140

Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys
 145 150 155 160

40 Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 1 | | 5 | | 10 | | 15 | | | | | | | | | |
| | Asn | Glu | Asp | Gly | Ser | Lys | Lys | Lys | Met | Ser | Thr | Thr | Ala | Lys | Val | Val |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| 5 | Ser | Ile | Ala | Thr | Val | Leu | Leu | Leu | Leu | Gly | Gly | Leu | Val | Phe | Ala | Ile |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| | Phe | Ala | Tyr | Val | Asp | His | Ser | Asn | Lys | Ala | Lys | Glu | Arg | Met | Leu | Asn |
| 10 | | 50 | | | | | 55 | | | | | 60 | | | | |
| | Glu | Gln | Lys | Gln | Glu | Gln | Lys | Glu | Lys | Arg | Gln | Lys | Glu | Asn | Ala | Glu |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| | Lys | Glu | Arg | Lys | Lys | Lys | Gln | Gln | Glu | Glu | Lys | Glu | Gln | Asn | Glu | Leu |
| 15 | | | | | | 85 | | | | 90 | | | | | 95 | |
| | Asp | Ser | Gln | Ala | Asn | Gln | Tyr | Gln | Gln | Leu | Pro | Gln | Gln | Asn | Gln | Tyr |
| | | | | 100 | | | | | | 105 | | | | 110 | | |
| 20 | Gln | Tyr | Val | Pro | Pro | Gln | Gln | Gln | Ala | Pro | Thr | Lys | Gln | Arg | Pro | Ala |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| | Lys | Glu | Glu | Asn | Asp | Asp | Lys | Ala | Ser | Lys | Asp | Glu | Ser | Lys | Asp | Lys |
| | | 130 | | | | | 135 | | | | | 140 | | | | |
| 25 | Asp | Asp | Lys | Ala | Ser | Gln | Asp | Lys | Ser | Asp | Asp | Asn | Gln | Lys | Lys | Thr |
| | 145 | | | | | 150 | | | | 155 | | | | | | 160 |
| | Asp | Asp | Asn | Lys | Gln | Pro | Ala | | | | | | | | | |
| 30 | | | | | | 165 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 45 | Met | Lys | Arg | Asn | Phe | Pro | Lys | Leu | Ile | Ala | Leu | Ser | Leu | Ile | Phe | Ser |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | Leu | Ser | Val | Thr | Pro | Ile | Ala | Asn | Ala | Glu | Ser | Asn | Ser | Asn | Ile | Lys |
| 50 | | | | 20 | | | | | 25 | | | | | 30 | | |
| | Ala | Lys | Asp | Lys | Lys | His | Val | Gln | Val | Asn | Val | Glu | Asp | Lys | Ser | Val |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| 55 | Pro | Thr | Asp | Val | Arg | Asn | Leu | Ala | Gln | Lys | Asp | Tyr | Leu | Ser | Tyr | Val |
| | 50 | | | | | 55 | | | | | | 60 | | | | |

[illegible]

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Lys | Met | Gln | Glu | Val | Lys | Tyr | Met | Thr | Glu | Ile | Thr | Phe | Lys |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Gly | Gly | Pro | Ile | His | Leu | Lys | Gly | Gln | Gln | Ile | Asn | Glu | Gly | Asp | Phe |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Ala | Pro | Asp | Phe | Thr | Val | Leu | Asp | Asn | Asp | Leu | Asn | Gln | Val | Thr | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Asp | Tyr | Ala | Gly | Lys | Lys | Lys | Leu | Ile | Ser | Val | Val | Pro | Ser | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asp | Thr | Gly | Val | Cys | Asp | Gln | Gln | Thr | Arg | Lys | Phe | Asn | Ser | Asp | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Lys | Glu | Glu | Gly | Ile | Val | Leu | Thr | Ile | Ser | Ala | Asp | Leu | Pro | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Gln | Lys | Arg | Trp | Cys | Ala | Ser | Ala | Gly | Leu | Asp | Asn | Val | Ile | Thr |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Leu | Ser | Asp | His | Arg | Asp | Leu | Ser | Phe | Gly | Glu | Asn | Tyr | Gly | Val | Val |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Met | Glu | Glu | Leu | Arg | Leu | Leu | Ala | Arg | Ala | Val | Phe | Val | Leu | Asp | Ala |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asp | Asn | Lys | Val | Val | Tyr | Lys | Glu | Ile | Val | Ser | Glu | Gly | Thr | Asp | Phe |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Pro | Asp | Phe | Asp | Ala | Ala | Leu | Ala | Ala | Tyr | Lys | Asn | Ile | | | |
| | | | | 165 | | | | | 170 | | | | | | |

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Glu | Ser | Arg | Phe | Ile | Met | Ala | Lys | Ile | Asn | Phe | Asp | Ala | Ala | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Gly | Asn | Pro | Gly | Ile | Ser | Thr | Cys | Ala | Ile | Val | Ile | Lys | Glu | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Gln | His | Tyr | Thr | Tyr | Thr | His | Glu | Leu | Gly | Glu | Met | Asp | Asn | His |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Ala | Glu | Trp | Ala | Ala | Cys | Ile | Tyr | Ala | Leu | Glu | His | Ala | Arg | Glu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Leu | Asn | Val | Gln | Asn | Ala | Leu | Leu | Tyr | Thr | Asp | Ser | Lys | Leu | Ile | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Asp | Ser | Ile | Glu | Ala | Gly | Tyr | Val | Lys | Asn | Ala | Asn | Phe | Lys | Pro | Tyr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Phe | Asp | Gln | Ile | Glu | Ile | Phe | Glu | Lys | Asp | Phe | Asp | Leu | Leu | Phe | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Lys | Trp | Ile | Pro | Arg | Glu | Gln | Asn | Lys | Glu | Ala | Asn | Gln | His | Ala | Gln |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Ala | Leu | Tyr | Lys | Leu | Ile | Lys | Lys | Asn | Lys | | | | | |
| | | 130 | | | | 135 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Thr | Val | Leu | Asp | Pro | Gln | Met | Ile | Lys | Asn | Glu | Asp | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

EP 0 786 519 A2

| | 20 | 25 | 30 |
|----|------------------------------------------------------------------------------------|----|----|
| 5 | Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp 35 40 45 | | |
| | Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile 50 55 60 | | |
| 10 | Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn 65 70 75 80 | | |
| | Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu 85 90 95 | | |
| 15 | Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys 100 105 110 | | |
| | Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu 115 120 125 | | |
| 20 | Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu 130 135 140 | | |
| | Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile 145 150 155 160 | | |
| 25 | Met Gln | | |

(2) INFORMATION FOR SEQ ID NO:5221:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

| | |
|----|--------------------------------------------------------------------------------|
| 45 | Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu 1 5 10 15 |
| | Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn 20 25 30 |
| 50 | Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu 35 40 45 |
| | Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys 50 55 60 |
| 55 | Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg 65 70 75 80 |

EP 0 786 519 A2

| | 85 | 90 | 95 |
|----|------------------------------------------------------------------------------------|----|----|
| 5 | Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp 100 105 110 | | |
| | Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn 115 120 125 | | |
| 10 | Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His 130 135 140 | | |
| | Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn 145 150 155 160 | | |
| 15 | Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr 165 170 175 | | |
| | Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala 180 185 190 | | |
| 20 | Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn 195 200 205 | | |
| | Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu 210 215 220 | | |
| 25 | Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile 225 230 235 240 | | |
| | Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys 245 250 255 | | |
| 30 | Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp 260 265 270 | | |
| | Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys 275 280 285 | | |
| 35 | Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys 290 295 300 | | |
| 40 | Tyr Gln Asn Lys Leu Ala Ser 305 310 | | |

(2) INFORMATION FOR SEQ ID NO:5222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 1 | | 5 | | 10 | | 15 | | | | | | | | | |
| | Glu | Gln | Leu | Tyr | Gly | Glu | Leu | Ile | Thr | Ala | Asn | Ile | Tyr | Arg | Ile | Lys |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| 5 | Gln | Gly | Asp | Lys | Glu | Val | Thr | Ala | Leu | Asn | Tyr | Tyr | Thr | Asn | Glu | Glu |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| 10 | Val | Val | Ile | Pro | Leu | Asn | Pro | Thr | Lys | Ser | Pro | Ser | Ala | Asn | Ala | Gln |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| | Tyr | Tyr | Tyr | Lys | Gln | Tyr | Xaa | Arg | Met | Lys | Thr | Arg | Xaa | Arg | Glu | Leu |
| | 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| 15 | Gln | His | Gln | Ile | Gln | Leu | Thr | Lys | Asp | Asn | Ile | Asp | Tyr | Phe | Ser | Thr |
| | | | | | 85 | | | | | 90 | | | | | 95 | |
| | Ile | Glu | Gln | Gln | Leu | His | His | Ile | Ser | Val | His | Asp | Ile | Asp | Glu | Ile |
| | | | | | 100 | | | | 105 | | | | | 110 | | |
| 20 | Arg | Asp | Glu | Leu | Ala | Glu | Gln | Gly | Phe | Met | Lys | Gln | Arg | Lys | Asn | Gln |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| | Thr | Lys | Lys | Lys | Lys | Ala | Gln | Ile | Gln | Leu | Gln | His | Tyr | Val | Ser | Thr |
| 25 | | 130 | | | | | 135 | | | | | 140 | | | | |
| | Asp | Gly | Asp | Asp | Ile | Tyr | Val | Gly | Lys | Asn | Asn | Lys | Gln | Asn | Asp | Tyr |
| | 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| 30 | Leu | Thr | Asn | Lys | Lys | Ala | Lys | Lys | Thr | His | Thr | Trp | Leu | His | Thr | Lys |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| | Asp | Ile | Pro | Gly | Ser | His | Val | Val | Ile | Phe | Asn | Asp | Ala | Pro | Ser | Asp |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| 35 | Thr | Thr | Ile | Lys | Glu | Ala | Ala | Met | Leu | Ala | Gly | Tyr | Phe | Ser | Lys | Ala |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| | Gly | Asn | Ser | Gly | Gln | Ile | Pro | Val | Asp | Tyr | Thr | Leu | Ile | Lys | Asn | Val |
| 40 | | 210 | | | | | 215 | | | | | 220 | | | | |
| | His | Lys | Pro | Ser | Gly | Ala | Lys | Pro | Gly | Phe | Val | Thr | Tyr | Asp | Asn | Gln |
| | 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| 45 | Lys | Thr | Leu | Tyr | Ala | | | | | | | | | | | |
| | | | | | 245 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 10 35 40 45
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 15 65 70 75 80
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95
 20 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
 1 5 10 15
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
 40 20 25 30
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
 35 40 45
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
 45 50 55 60
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
 50 65 70 75 80
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
 85 90 95
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
 55 100 105 110

115

120

125

His Ser Ile

130

5

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

20

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

25

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

30

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

35

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

40

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

45

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

50

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

55

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

EP 0 786 519 A2

| | 210 | | 215 | | 220 |
|----|-----------------------------------------------------------------|-----|-----|-----|---------|
| | Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly | | | | |
| | 225 | | 230 | | 235 240 |
| 5 | Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn | | | | |
| | | 245 | | 250 | 255 |
| | Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val | | | | |
| 10 | | 260 | | 265 | 270 |
| | Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys | | | | |
| | | 275 | | 280 | 285 |
| 15 | Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr | | | | |
| | | 290 | | 295 | 300 |
| | Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp | | | | |
| | | 305 | | 310 | 315 320 |
| 20 | Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly | | | | |
| | | 325 | | 330 | 335 |
| | Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu | | | | |
| | | 340 | | 345 | 350 |
| 25 | Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr | | | | |
| | | 355 | | 360 | 365 |
| | Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly | | | | |
| 30 | | 370 | | 375 | 380 |
| | Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro | | | | |
| | | 385 | | 390 | 395 400 |
| 35 | Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn | | | | |
| | | 405 | | 410 | 415 |
| | Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu | | | | |
| | | 420 | | 425 | 430 |
| 40 | Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr | | | | |
| | | 435 | | 440 | 445 |
| | Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr | | | | |
| | | 450 | | 455 | 460 |
| 45 | Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly | | | | |
| | | 465 | | 470 | 475 480 |
| | Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp | | | | |
| 50 | | 485 | | 490 | 495 |
| | Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr | | | | |
| | | 500 | | 505 | 510 |
| 55 | Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser | | | | |
| | | 515 | | 520 | 525 |

530

535

540

(2) INFORMATION FOR SEQ ID NO:5226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
 1 5 10 15
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
 20 25 30
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
 35 40 45
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
 50 55 60
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
 65 70 75 80
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
 85 90 95
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
 100 105 110
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
 115 120 125
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
 130 135 140
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
 145 150 155 160
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
 165 170 175
 Lys

(2) INFORMATION FOR SEQ ID NO:5227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

10

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
1 5 10 15

Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
20 25 30

15

His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
35 40 45

Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
50 55 60

20

Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
65 70 75 80

Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
85 90 95

25

Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
100 105 110

Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
115 120 125

30

Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
130 135 140

35

Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
145 150 155 160

Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
165 170 175

40

Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
180 185 190

Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
195 200 205

45

Cys

(2) INFORMATION FOR SEQ ID NO:5228:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

| | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5 | Thr | Phe | Arg | Ile | Ile | Phe | Leu | Leu | Ser | Ile | Arg | Lys | Arg | Ser | Asn | Arg | 1 | 5 | 10 | 15 |
| | Thr | His | Val | Ser | Ile | His | Trp | Ser | Thr | Val | Asn | Lys | Glu | Glu | Ile | Cys | 20 | 25 | 30 | |
| 10 | Leu | Arg | Val | Lys | Asp | Asn | Leu | Gln | Gln | Ile | Ser | Thr | Gln | Ile | Asn | Asp | 35 | 40 | 45 | |
| | Lys | Ser | Glu | Lys | Asn | Asn | Phe | Ser | Thr | Lys | Pro | Asn | Val | Ile | Ala | Val | 50 | 55 | 60 | |
| 15 | Thr | Lys | Tyr | Val | Thr | Ile | Glu | Arg | Ala | Lys | Glu | Ala | Tyr | Glu | Ala | Gly | 65 | 70 | 75 | 80 |
| | Ile | Arg | His | Phe | Gly | Glu | Asn | Arg | Leu | Glu | Gly | Phe | Phe | Gln | Lys | Lys | 85 | 90 | 95 | |
| 20 | Glu | Ala | Leu | Pro | Ser | Asp | Ala | Val | Ile | His | Phe | Ile | Gly | Ser | Leu | Gln | 100 | 105 | 110 | |
| | Ser | Arg | Lys | Val | Lys | Asp | Val | Ile | Asn | Asp | Val | Asp | Tyr | Phe | His | Ala | 115 | 120 | 125 | |
| 25 | Leu | Asp | Arg | Leu | Ser | Leu | Ala | Lys | Glu | Ile | Asn | Lys | Arg | Ala | Glu | His | 130 | 135 | 140 | |
| 30 | Lys | Ile | Lys | Cys | Phe | Leu | Gln | Val | Asn | Val | Ser | Gly | Glu | Ala | Ser | Lys | 145 | 150 | 155 | 160 |
| | His | Gly | Ile | Ala | Leu | Glu | Asp | Val | Asp | Gln | Phe | Ile | Asp | Asp | Leu | Lys | 165 | 170 | 175 | |
| 35 | Lys | Tyr | Asp | Lys | Ile | Glu | Ile | Val | Gly | Leu | Met | Thr | Met | Ala | Pro | Leu | 180 | 185 | 190 | |
| | Thr | Asp | Asp | Glu | Ala | Tyr | Ile | Arg | Ser | Leu | Phe | Lys | Gln | Leu | Arg | Leu | 195 | 200 | 205 | |
| 40 | Lys | Lys | Glu | Glu | Ile | Gln | Arg | Leu | Asn | Leu | Glu | Tyr | Ala | Pro | Cys | Asp | 210 | 215 | 220 | |
| | Glu | Leu | Ser | Met | Gly | Met | Ser | Asn | Asp | Tyr | Leu | Ile | Ala | Val | Glu | Glu | 225 | 230 | 235 | 240 |
| 45 | Gly | Ala | Thr | Phe | Val | Arg | Ile | Gly | Thr | Lys | Leu | Val | Gly | Glu | Glu | Glu | 245 | 250 | 255 | |

50

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
 195 200 205
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
 210 215 220
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
 225 230 235 240
 Leu Gly Ala Trp Gly Phe
 245

55

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Lys | Glu | Pro | His | Lys | Met | Lys | Lys | Ile | Tyr | Lys | Ser | Leu | Thr | Val | Ser | 1 | 5 | 10 | 15 |
| Ala | Ile | Val | Ala | Thr | Val | Ser | Leu | Ser | Ala | Leu | Pro | Gln | Ser | Leu | Ala | 20 | 25 | 30 | |
| Ile | Thr | His | Glu | Ser | Gln | Pro | Thr | Lys | Gln | Gln | Arg | Thr | Val | Leu | Phe | 35 | 40 | 45 | |
| Asp | Arg | Ser | His | Gly | Gln | Thr | Ala | Gly | Ala | Ala | Asp | Trp | Val | Ser | Asp | 50 | 55 | 60 | |
| Gly | Ala | Phe | Ser | Asp | Tyr | Ala | Asp | Ser | Ile | Gln | Lys | Gln | Gly | Tyr | Asp | 65 | 70 | 75 | |
| Val | Lys | Ala | Ile | Asp | Gly | His | Ser | Asn | Ile | Thr | Glu | Ala | Ser | Leu | Lys | 85 | 90 | 95 | |
| Ser | Ser | Lys | Ile | Phe | Val | Ile | Pro | Glu | Ala | Asn | Ile | Pro | Phe | Lys | Glu | 100 | 105 | 110 | |
| Ser | Glu | Gln | Ala | Ala | Ile | Val | Lys | Tyr | Val | Lys | Gln | Gly | Gly | Asn | Val | 115 | 120 | 125 | |
| Val | Phe | Ile | Ser | Asp | His | Tyr | Asn | Ala | Asp | Arg | Asn | Leu | Asn | Arg | Ile | 130 | 135 | 140 | |
| Asp | Ser | Ser | Glu | Ala | Met | Asn | Gly | Tyr | Arg | Arg | Gly | Ala | Tyr | Glu | Asp | 145 | 150 | 155 | |
| Met | Ser | Lys | Gly | Met | Asn | Ala | Glu | Glu | Lys | Ser | Ser | Thr | Ala | Met | Gln | 165 | 170 | 175 | |
| Gly | Val | Lys | Ser | Ser | Asp | Trp | Leu | Ser | Thr | Asn | Phe | Gly | Val | Arg | Phe | 180 | 185 | 190 | |
| Arg | Tyr | Asn | Ala | Leu | Gly | Asp | Leu | Asn | Thr | Ser | Asn | Ile | Val | Ser | Ser | 195 | 200 | 205 | |
| Lys | Glu | Ser | Phe | Gly | Ile | Thr | Glu | Gly | Val | Lys | Ser | Val | Ser | Met | His | 210 | 215 | 220 | |
| Ala | Gly | Ser | Thr | Leu | Ala | Ile | Thr | Asn | Pro | Glu | Lys | Ala | Lys | Gly | Ile | 225 | 230 | 235 | |
| Val | Tyr | Thr | Pro | Glu | Gln | Leu | Pro | Ala | Lys | Ser | Lys | Trp | Ser | His | Ala | 245 | 250 | 255 | |

EP 0 786 519 A2

Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
260 265 270

5 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
275 280 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
290 295 300

10 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
305 310 315 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
325 330 335

15 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
340 345 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
355 360 365

20 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
370 375 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
385 390 395 400

Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
405 410 415

30 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
420 425 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
435 440 445

35 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
450 455 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
465 470 475 480

40 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
485 490 495

Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
500 505 510

45 Leu Ile Thr Thr Asp Phe Lys
515

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

| | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|-----|-----|-----|
| 5 | Arg | Asp | Glu | Arg | Ile | Lys | Thr | Met | Thr | Asn | Ser | Ser | Lys | Ser | Phe | Thr | 1 | -5- | 10 | 15 |
| | Lys | Phe | Met | Ala | Ala | Ser | Ala | Val | Phe | Thr | Met | Gly | Phe | Leu | Ser | Val | | 20 | 25 | 30 |
| 10 | Pro | Thr | Ala | Gly | Ala | Glu | Gln | Thr | Asn | Gln | Ile | Ala | Asn | Lys | Pro | Gln | | 35 | 40 | 45 |
| | Ala | Ile | Gln | Trp | His | Thr | Asn | Leu | Thr | Asn | Glu | Arg | Phe | Thr | Thr | Ile | | 50 | 55 | 60 |
| 15 | Ala | His | Arg | Gly | Ala | Ser | Gly | Tyr | Ala | Pro | Glu | His | Thr | Phe | Gln | Ala | | 65 | 70 | 75 |
| | Tyr | Asp | Lys | Ser | His | Asn | Glu | Leu | Lys | Ala | Ser | Tyr | Ile | Glu | Ile | Asp | | 85 | 90 | 95 |
| 20 | Leu | Gln | Arg | Thr | Lys | Asp | Gly | His | Leu | Val | Ala | Met | His | Asp | Glu | Thr | | 100 | 105 | 110 |
| 25 | Val | Asn | Arg | Thr | Thr | Asn | Gly | His | Gly | Lys | Val | Glu | Asp | Tyr | Thr | Leu | | 115 | 120 | 125 |
| | Asp | Glu | Leu | Lys | Gln | Leu | Asp | Ala | Gly | Ser | Trp | Phe | Asn | Lys | Lys | Tyr | | 130 | 135 | 140 |
| 30 | Pro | Lys | Tyr | Ala | Arg | Ala | Ser | Tyr | Lys | Asn | Ala | Lys | Val | Pro | Thr | Leu | | 145 | 150 | 155 |
| | Asp | Glu | Ile | Leu | Glu | Arg | Tyr | Gly | Pro | Asn | Ala | Asn | Tyr | Tyr | Ile | Glu | | 165 | 170 | 175 |
| 35 | Thr | Lys | Ser | Pro | Asp | Val | Tyr | Pro | Gly | Met | Glu | Glu | Gln | Leu | Leu | Ala | | 180 | 185 | 190 |
| 40 | Ser | Leu | Lys | Lys | His | His | Leu | Leu | Asn | Asn | Asn | Lys | Leu | Lys | Asn | Gly | | 195 | 200 | 205 |
| | His | Val | Met | Ile | Gln | Ser | Phe | Ser | Asp | Glu | Ser | Leu | Lys | Lys | Ile | His | | 210 | 215 | 220 |
| 45 | Arg | Gln | Asn | Lys | His | Val | Pro | Leu | Val | Lys | Leu | Val | Asp | Lys | Gly | Glu | | 225 | 230 | 235 |
| | Leu | Gln | Gln | Phe | Asn | Asp | Gln | Arg | Leu | Lys | Glu | Ile | Arg | Ser | Tyr | Ala | | 245 | 250 | 255 |
| 50 | Ile | Gly | Leu | Gly | Pro | Asp | Tyr | Thr | Asp | Leu | Thr | Glu | Gln | Asn | Thr | His | | 260 | 265 | 270 |
| 55 | His | Leu | Lys | Asp | Leu | Gly | Phe | Ile | Val | His | Pro | Tyr | Thr | Val | Asn | Glu | | 275 | 280 | 285 |

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
 290 295 300

5 Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

20 Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
 1 5 10 15
 25 Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
 20 25 30
 Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
 35 40 45
 30 Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
 50 55 60
 Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
 65 70 75 80
 35 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
 85 90 95
 Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
 100 105 110
 40 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
 115 120 125
 Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
 130 135 140
 45 Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
 145 150 155 160
 Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
 50 165 170 175
 His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
 180 185 190
 55 Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
 195 200 205

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Asp | Tyr | Ala | Ile | Leu | Asp | Leu | His | Val | Ile | Lys | Glu | Thr | Pro | Lys | Ile |
| | 210 | | | | | | 215 | | | | | 220 | | | | |
| 5 | Leu | Asp | Phe | Thr | Lys | Gln | Leu | Ala | Pro | Thr | Thr | His | Ala | Val | Thr | Tyr |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| | Tyr | Thr | Phe | Asn | Phe | Ser | Leu | Glu | Gly | Ala | Lys | Met | Ser | Leu | Pro | Gly |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| 10 | Thr | Asp | Gly | Leu | Lys | Thr | Gly | Ser | Ser | Asp | Thr | Ala | Asn | Tyr | Asn | His |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| | Thr | Ile | Thr | Thr | Lys | Arg | Gly | Lys | Phe | Arg | Ile | Asn | Gln | Val | Ile | Met |
| | | | 275 | | | | | 280 | | | | | 285 | | | |
| 15 | Gly | Ala | Gly | Asp | Tyr | Lys | Asn | Leu | Gly | Gly | Glu | Lys | Gln | Arg | Asn | Met |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| | Met | Gly | Asn | Ala | Leu | Met | Glu | Arg | Ser | Phe | Asp | Gln | Tyr | Lys | Tyr | Val |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| 20 | Lys | Ile | Leu | Ser | Lys | Gly | Glu | Gln | Arg | Ile | Asn | Gly | Lys | Lys | Tyr | Tyr |
| | | | | | 325 | | | | | 330 | | | | | 335 | |
| | Val | Glu | Asn | Asp | Leu | Tyr | Asp | Val | Leu | Pro | Ser | Asp | Phe | Ser | Lys | Lys |
| 25 | | | | 340 | | | | | 345 | | | | | 350 | | |
| | Asp | Tyr | Lys | Leu | Val | Val | Glu | Asp | Gly | Lys | Val | His | Ala | Asp | Tyr | Pro |
| | | | 355 | | | | | 360 | | | | | 365 | | | |
| 30 | Arg | Glu | Phe | Ile | Asn | Lys | Asp | Tyr | Gly | Pro | Pro | Thr | Val | Glu | Val | His |
| | 370 | | | | | | 375 | | | | | 380 | | | | |
| | Gln | Pro | Ile | Ile | Gln | Lys | Ala | Asn | Thr | Val | Ala | Lys | Ser | Met | Trp | Glu |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| 35 | Glu | His | Pro | Leu | Phe | Thr | Ile | Ile | Gly | Gly | Thr | Cys | Leu | Val | Ala | Gly |
| | | | | | 405 | | | | | 410 | | | | | 415 | |
| | Leu | Ala | Leu | Ile | Val | His | Met | Ile | Ile | Asn | Arg | Leu | Phe | Arg | Lys | Arg |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| 40 | Lys | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5233:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

EP 0 786 519 A2

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
1 5 10 15

Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
5 20 25 30

Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
35 40 45

Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
10 50 55 60

Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
65 70 75 80

Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
15 85 90 95

Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
100 105 110

Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
115 120 125

Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
25 130 135 140

Asp Ile Asn Val Lys Thr Lys
145 150

(2) INFORMATION FOR SEQ ID NO:5234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
1 5 10 15

Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
20 25 30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
35 40 45

Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
50 55 60

Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
55 65 70 75 80

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Val | His | Asn | Glu | Ser | Gln | Thr | Ser | Glu | Asp | Asn | Val | Gln | Asn | Glu | Ala | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 5 | Gly | Thr | Ile | Asp | Asp | Arg | Gln | Val | Glu | Ser | Ser | His | Ser | Thr | Glu | Ser | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Gln | Glu | Pro | Ser | His | Gln | Asp | Ser | Thr | Pro | Gln | His | Glu | Glu | Glu | Tyr | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 10 | Tyr | Asn | Lys | Asn | Ala | Phe | Ala | Met | Asp | Lys | Ser | His | Pro | Glu | Pro | Ile | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Glu | Asp | Asn | Asp | Lys | His | Asp | Thr | Ile | Lys | Asn | Ala | Glu | Asn | Asn | Thr | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 15 | Glu | His | Ser | Thr | Val | Ser | Asp | Lys | Ser | Glu | Ala | Glu | Gln | Ser | Gln | Gln | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| | Pro | Lys | Pro | Tyr | Phe | Thr | Thr | Gly | Ala | Asn | Gln | Ser | Glu | Thr | Ser | Lys | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 20 | Asn | Glu | His | Asp | Asn | Asp | Ser | Val | Lys | Gln | Asp | Gln | Asp | Glu | Pro | Lys | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| | Glu | His | His | Asn | Gly | Lys | Lys | Ala | Ala | Ala | Ile | Gly | Ala | Gly | Thr | Ala | |
| 25 | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Gly | Val | Ala | Gly | Ala | Ala | Gly | Ala | Met | Ala | Ala | Ser | Lys | Ala | Lys | Lys | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| | His | Ser | Asn | Asp | Ala | Gln | Asn | Lys | Ser | Asn | Ser | Gly | Lys | Ala | Asn | Asn | |
| 30 | | | | | 245 | | | | | 250 | | | | | 255 | | |
| | Ser | Thr | Glu | Asp | Lys | Ala | Ser | Gln | Asp | Lys | Ser | Lys | Asp | His | His | Asn | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 35 | Gly | Lys | Lys | Gly | Ala | Ala | Ile | Gly | Ala | Gly | Thr | Ala | Gly | Leu | Ala | Gly | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| | Gly | Ala | Ala | Ser | Lys | Ser | Ala | Ser | Ala | Ala | Ser | Lys | Pro | His | Ala | Ser | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 40 | Asn | Asn | Ala | Ser | Gln | Asn | His | Asp | Glu | His | Asp | Asn | His | Asp | Arg | Asp | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| | Lys | Glu | Arg | Lys | Lys | Gly | Gly | Met | Ala | Lys | Val | Leu | Leu | Pro | Leu | Ile | |
| 45 | | | | | 325 | | | | | 330 | | | | | 335 | | |
| | Ala | Ala | Val | Leu | Ile | Ile | Gly | Ala | Leu | Ala | Ile | Phe | Gly | Gly | Met | Ala | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| | Leu | Asn | Asn | His | Asn | Asn | Gly | Thr | Lys | Glu | Asn | Lys | Ile | Ala | Asn | Thr | |
| 50 | | | 355 | | | | | 360 | | | | | 365 | | | | |
| | Asn | Lys | Asn | Asn | Ala | Asp | Glu | Ser | Lys | Asp | Lys | Asp | Thr | Ser | Lys | Asp | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |
| 55 | Ala | Ser | Lys | Asp | Lys | Ser | Lys | Ser | Thr | Asp | Ser | Asp | Lys | Ser | Lys | Glu | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |

EP 0 786 519 A2

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn
405 410 415

Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln
5 420 425 430

Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln
435 440 445

Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln
10 450 455 460

Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala
465 470 475 480

Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile
15 485 490 495

Pro

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn
1 5 10 15

Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr
20 25 30

Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser
35 40 45

Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile
50 55 60

Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp
65 70 75 80

Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn
85 90 95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
100 105 110

Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
115 120 125

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Gln | Leu | Leu | Asp | Lys | Asn | Asn | Glu | Thr | Gln | Tyr | Tyr | His | Phe | Phe | Ser |
| | 130 | | | | | | 135 | | | | | 140 | | | | |
| 5 | Ile | Lys | Asp | Pro | Ala | Asp | Val | Tyr | Tyr | Thr | Lys | Lys | Lys | Ala | Glu | Val |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| | Glu | Leu | Asp | Ile | Asn | Thr | Ala | Ser | Thr | Trp | Lys | Lys | Phe | Glu | Val | Tyr |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| 10 | Glu | Asn | Asn | Gln | Lys | Leu | Pro | Val | Arg | Leu | Val | Ser | Tyr | Ser | Pro | Val |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| | Pro | Glu | Asp | His | Ala | Tyr | Ile | Arg | Phe | Pro | Val | Ser | Asp | Gly | Thr | Gln |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| 15 | Glu | Leu | Lys | Ile | Val | Ser | Ser | Thr | Gln | Ile | Asp | Asp | Gly | Glu | Glu | Thr |
| | 210 | | | | | | 215 | | | | | 220 | | | | |
| | Asn | Tyr | Asp | Tyr | Thr | Lys | Leu | Val | Phe | Ala | Lys | Pro | Ile | Tyr | Asn | Asp |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| 20 | Pro | Ser | Leu | Val | Lys | Ser | Asp | Thr | Asn | Asp | Ala | Val | Val | Thr | Asn | Asp |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| | Gln | Ser | Ser | Ser | Val | Ala | Ser | Asn | Gln | Thr | Asn | Thr | Asn | Thr | Ser | Asn |
| 25 | | | | | 260 | | | | 265 | | | | | 270 | | |
| | Gln | Asn | Ile | Ser | Thr | Ile | Asn | Asn | Ala | Asn | Asn | Gln | Pro | Gln | Ala | Thr |
| | | | 275 | | | | | 280 | | | | | 285 | | | |
| 30 | Thr | Asn | Met | Ser | Gln | Pro | Ala | Gln | Pro | Lys | Ser | Ser | Thr | Asn | Ala | Asp |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| | Gln | Ala | Ser | Ser | Gln | Pro | Ala | His | Glu | Thr | Asn | Ser | Asn | Gly | Asn | Thr |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| 35 | Asn | Asp | Lys | Thr | Asn | Glu | Ser | Ser | Asn | Gln | Ser | Asp | Val | Asn | Gln | Gln |
| | | | | | 325 | | | | | 330 | | | | | 335 | |
| | Tyr | Pro | Pro | Ala | Asp | Glu | Ser | Leu | Gln | Asp | Ala | Ile | Lys | Asn | Pro | Ala |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| 40 | Ile | Ile | Asp | Lys | Glu | His | Thr | Ala | Asp | Asn | Trp | Arg | Pro | Ile | Asp | Phe |
| | | | 355 | | | | | 360 | | | | | 365 | | | |
| | Gln | Met | Lys | Asn | Asp | Lys | Gly | Glu | Arg | Gln | Phe | Tyr | His | Tyr | Ala | Ser |
| 45 | | | 370 | | | | 375 | | | | | 380 | | | | |
| | Thr | Val | Glu | Pro | Ala | Thr | Val | Ile | Phe | Thr | Lys | Thr | Gly | Pro | Ile | Ile |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| | Glu | Leu | Gly | Leu | Lys | Thr | Ala | Ser | Thr | Trp | Lys | Lys | Phe | Glu | Val | Tyr |
| 50 | | | | | 405 | | | | | 410 | | | | | 415 | |
| | Glu | Gly | Asp | Lys | Lys | Leu | Pro | Val | Glu | Leu | Val | Ser | Tyr | Asp | Ser | Asp |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| 55 | Lys | Asp | Tyr | Ala | Tyr | Ile | Arg | Phe | Pro | Val | Ser | Asn | Gly | Thr | Arg | Glu |
| | | | 435 | | | | | 440 | | | | | 445 | | | |

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Val | Lys | Ile | Val | Ser | Ser | Ile | Glu | Tyr | Gly | Glu | Asn | Ile | His | Glu | Asp | |
| | 450 | | | | | | 455 | | | | | 460 | | | | | |
| 5 | Tyr | Asp | Tyr | Thr | Leu | Met | Val | Phe | Ala | Gln | Pro | Ile | Thr | Asn | Asn | Pro | |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| | Asp | Asp | Tyr | Val | Asp | Glu | Glu | Thr | Tyr | Asn | Leu | Gln | Lys | Leu | Leu | Ala | |
| | | | | | 485 | | | | | 490 | | | | | 495 | | |
| 10 | Pro | Tyr | His | Lys | Ala | Lys | Thr | Leu | Glu | Arg | Gln | Val | Tyr | Glu | Leu | Glu | |
| | | | | 500 | | | | | 505 | | | | | 510 | | | |
| | Lys | Leu | Gln | Glu | Lys | Leu | Pro | Glu | Lys | Tyr | Lys | Ala | Glu | Tyr | Lys | Lys | |
| | | | 515 | | | | | 520 | | | | | 525 | | | | |
| 15 | Lys | Leu | Asp | Gln | Thr | Arg | Val | Glu | Leu | Ala | Asp | Gln | Val | Lys | Ser | Ala | |
| | 530 | | | | | | 535 | | | | | 540 | | | | | |
| | Val | Thr | Glu | Phe | Glu | Asn | Val | Thr | Pro | Thr | Asn | Asp | Gln | Leu | Thr | Asp | |
| | 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| 20 | Leu | Gln | Glu | Ala | His | Phe | Val | Val | Phe | Glu | Ser | Glu | Glu | Asn | Ser | Glu | |
| | | | | | 565 | | | | | 570 | | | | | 575 | | |
| | Ser | Val | Met | Asp | Gly | Phe | Val | Glu | His | Pro | Phe | Tyr | Thr | Ala | Thr | Leu | |
| 25 | | | | 580 | | | | | 585 | | | | | 590 | | | |
| | Asn | Gly | Gln | Lys | Tyr | Val | Val | Met | Lys | Thr | Lys | Asp | Asp | Ser | Tyr | Trp | |
| | | | 595 | | | | | 600 | | | | | 605 | | | | |
| 30 | Lys | Asp | Leu | Ile | Val | Glu | Gly | Lys | Arg | Val | Thr | Thr | Val | Ser | Lys | Asp | |
| | 610 | | | | | | 615 | | | | | 620 | | | | | |
| | Pro | Lys | Asn | Asn | Ser | Arg | Thr | Leu | Ile | Phe | Pro | Tyr | Ile | Pro | Asp | Lys | |
| | 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| 35 | Ala | Val | Tyr | Asn | Ala | Ile | Val | Lys | Val | Val | Val | Ala | Asn | Ile | Gly | Tyr | |
| | | | | | 645 | | | | | | 650 | | | | 655 | | |
| | Glu | Gly | Gln | Tyr | His | Val | Arg | Ile | Ile | Asn | Gln | Asp | Ile | Asn | Thr | Lys | |
| | | | | 660 | | | | | 665 | | | | | 670 | | | |
| 40 | Asp | Asp | Asp | Thr | Ser | Gln | Asn | Asn | Thr | Ser | Glu | Pro | Leu | Asn | Val | Gln | |
| | | | 675 | | | | | 680 | | | | | 685 | | | | |
| | Thr | Gly | Gln | Glu | Gly | Lys | Val | Ala | Asp | Thr | Asp | Val | Ala | Glu | Asn | Ser | |
| 45 | | | | | | | 695 | | | | | 700 | | | | | |
| | Ser | Thr | Ala | Thr | Asn | Pro | Lys | Asp | Ala | Ser | Asp | Lys | Ala | Asp | Val | Ile | |
| | 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| | Glu | Pro | Glu | Ser | Asp | Val | Val | Lys | Asp | Ala | Asp | Asn | Asn | Ile | Asp | Lys | |
| 50 | | | | | 725 | | | | | 730 | | | | | 735 | | |
| | Asp | Val | Gln | His | Asp | Val | Asp | His | Leu | Ser | Asp | Met | Ser | Asp | Asn | Asn | |
| | | | | 740 | | | | | 745 | | | | | 750 | | | |
| 55 | His | Phe | Asp | Lys | Tyr | Asp | Leu | Lys | Glu | Met | Asp | Thr | Gln | Ile | Ala | Lys | |
| | | | 755 | | | | | 760 | | | | | 765 | | | | |

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Asp | Thr | Asp | Arg | Asn | Val | Asp | Lys | Asp | Ala | Asp | Asn | Ser | Val | Gly | Met |
| | 770 | | | | | | 775 | | | | | 780 | | | | |
| 5 | Ser | Ser | Asn | Val | Asp | Thr | Asp | Lys | Asp | Ser | Asn | Lys | Asn | Lys | Asp | Lys |
| | 785 | | | | | 790 | | | | | 795 | | | | | 800 |
| | Val | Ile | Gln | Leu | Asn | His | Ile | Ala | Asp | Lys | Asn | Asn | His | Thr | Gly | Lys |
| | | | | | 805 | | | | | 810 | | | | | 815 | |
| 10 | Ala | Ala | Lys | Leu | Asp | Val | Val | Lys | Gln | Asn | Tyr | Asn | Asn | Thr | Asp | Lys |
| | | | | 820 | | | | | 825 | | | | | 830 | | |
| | Val | Thr | Asp | Lys | Lys | Thr | Thr | Glu | His | Leu | Pro | Ser | Asp | Ile | His | Lys |
| | | | 835 | | | | | 840 | | | | | 845 | | | |
| 15 | Thr | Val | Asp | Lys | Thr | Val | Lys | Thr | Lys | Glu | Lys | Ala | Gly | Thr | Pro | Ser |
| | 850 | | | | | | 855 | | | | | 860 | | | | |
| | Lys | Glu | Asn | Lys | Leu | Ser | Gln | Ser | Lys | Met | Leu | Thr | Lys | Asn | Trp | Arg |
| | 865 | | | | | 870 | | | | | 875 | | | | | 880 |
| 20 | Asn | Asn | Xaa | Gln | Ala | Asn | | | | | | | | | | |
| | | | | | 885 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Asn | Met | Asn | Lys | Asn | Val | Met | Val | Lys | Gly | Leu | Thr | Ala | Leu | Thr | Ile |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| 40 | Leu | Thr | Ser | Leu | Gly | Phe | Ala | Glu | Asn | Ile | Ser | Asn | Gln | Xaa | His | Ser |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| | Ile | Ala | Lys | Ala | Glu | Lys | Asn | Val | Lys | Glu | Ile | Thr | Asp | Ala | Thr | Lys |
| | | | 35 | | | | 40 | | | | | | 45 | | | |
| 45 | Glu | Pro | Tyr | Asn | Ser | Val | Val | Ala | Phe | Val | Gly | Gly | Thr | Gly | Val | Val |
| | 50 | | | | | | 55 | | | | 60 | | | | | |
| | Val | Gly | Lys | Asn | Thr | Ile | Val | Thr | Asn | Lys | His | Ile | Ala | Lys | Ser | Asn |
| 50 | 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| | Asp | Ile | Phe | Lys | Asn | Arg | Val | Ser | Ala | His | His | Ser | Ser | Lys | Gly | Lys |
| | | | | 85 | | | | | 90 | | | | | | 95 | |
| 55 | Gly | Gly | Gly | Asn | Tyr | Asp | Val | Lys | Asp | Ile | Val | Glu | Tyr | Pro | Gly | Lys |
| | | | | 100 | | | | | 105 | | | | | 110 | | |

EP 0 786 519 A2

Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
 115 120 125
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
 130 135 140
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
 145 150 155 160
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
 165 170 175
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
 180 185 190
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
 195 200 205
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
 210 215 220
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
 1 5 10 15
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
 20 25 30
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
 35 40 45
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
 50 55 60
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
 65 70 75 80
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
 85 90 95
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
 100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
 115 120 125
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
 130 135 140
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
 145 150 155 160
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
 165 170 175
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
 180 185 190
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
 195 200 205
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
 210 215 220
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val
 225 230 235 240
 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
 245 250 255
 25 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
 260 265 270
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
 275 280 285
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
 290 295 300
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
 305 310 315 320
 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
 325 330 335
 40 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
 340 345 350
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
 1 5 10 15
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
 20 25 30
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
 35 40 45
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
 50 55 60
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
 65 70 75 80
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
 85 90 95
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
 100 105 110
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
 115 120 125
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
 130 135 140
 Val Asp Thr Lys Lys Gln
 145 150
 30

(2) INFORMATION FOR SEQ ID NO:5239:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
 1 5 10 15
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
 20 25 30
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
 35 40 45
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly
 50 55 60
 55

EP 0 786 519 A2

Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
65 70 75 80

Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
5 85 90 95

Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
100 105 110

Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
10 115 120 125

Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
130 135 140

Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
15 145 150 155 160

Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
165 170 175

Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
180 185 190

Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
195 200 205

Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
210 215 220

Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
225 230 235

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
1 5 10 15

Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
20 25 30

Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
35 40 45

Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
50 55 60

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
65 70 75 80

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe
100 105 110

Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
115 120 125

Phe Asp Val Lys Ala
130

(2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly
20 25 30

Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
50 55 60

Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
85 90 95

Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
100 105 110

Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
130 135 140

Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
145 150 155 160

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Pro | Ile | Gly | Val | Val | Gly | Ala | Val | Val | Ala | Trp | Asn | Phe | Pro | Met | Leu | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 5 | Leu | Ala | Ala | Trp | Lys | Ile | Ala | Pro | Ala | Ile | Ala | Ala | Gly | Asn | Thr | Ile | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Val | Ile | Gln | Pro | Ser | Ser | Ser | Thr | Pro | Leu | Ser | Leu | Leu | Glu | Val | Ala | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 10 | Lys | Ile | Phe | Gln | Glu | Val | Leu | Pro | Lys | Gly | Val | Val | Asn | Ile | Leu | Thr | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Gly | Lys | Gly | Ser | Glu | Ser | Gly | Asn | Ala | Ile | Phe | Asn | His | Asp | Gly | Val | |
| | | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| 15 | Asp | Lys | Leu | Ser | Phe | Thr | Gly | Ser | Thr | Asp | Val | Gly | Tyr | Gln | Val | Ala | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| | Glu | Ala | Ala | Ala | Lys | His | Leu | Val | Pro | Ala | Thr | Leu | Glu | Leu | Gly | Gly | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 20 | Lys | Ser | Ala | Asn | Ile | Ile | Leu | Asp | Asp | Ala | Asn | Leu | Asp | Leu | Ala | Val | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| | Glu | Gly | Ile | Gln | Leu | Gly | Ile | Leu | Phe | Asn | Gln | Gly | Glu | Val | Cys | Ser | |
| 25 | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | Ala | Gly | Ser | Arg | Leu | Leu | Val | His | Glu | Lys | Ile | Tyr | Asp | Gln | Leu | Val | |
| | | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| | Pro | Arg | Leu | Gln | Glu | Ala | Phe | Ser | Asn | Ile | Lys | Val | Gly | Asn | Pro | Gln | |
| 30 | | | | 325 | | | | | | 330 | | | | | 335 | | |
| | Asp | Glu | Ala | Thr | Gln | Met | Gly | Ser | Gln | Thr | Gly | Lys | Asp | Gln | Leu | Asp | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| 35 | Lys | Ile | Gln | Ser | Tyr | Ile | Asp | Ala | Ala | Lys | Glu | Ser | Asp | Ala | Gln | Ile | |
| | | | 355 | | | | 360 | | | | | | 365 | | | | |
| | Leu | Ala | Gly | Gly | His | Arg | Leu | Thr | Glu | Asn | Gly | Leu | Asp | Lys | Gly | Phe | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |
| 40 | Phe | Phe | Glu | Pro | Thr | Leu | Ile | Ala | Val | Pro | Asp | Asn | His | His | Lys | Leu | |
| | | 385 | | | | 390 | | | | | 395 | | | | | 400 | |
| | Ala | Gln | Glu | Glu | Ile | Phe | Gly | Pro | Val | Leu | Thr | Val | Ile | Lys | Val | Lys | |
| | | | | 405 | | | | | | 410 | | | | | 415 | | |
| 45 | Asp | Asp | Gln | Glu | Ala | Ile | Asp | Ile | Ala | Asn | Asp | Ser | Glu | Tyr | Gly | Leu | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | |
| | Ala | Gly | Gly | Val | Phe | Ser | Gln | Asn | Ile | Thr | Arg | Ala | Leu | Asn | Ile | Ala | |
| | | | 435 | | | | | 440 | | | | | 445 | | | | |
| 50 | Lys | Ala | Val | Arg | Thr | Gly | Arg | Ile | Trp | Ile | Asn | Thr | Tyr | Asn | Gln | Val | |
| | | 450 | | | | | 455 | | | | | 460 | | | | | |
| | Pro | Glu | Gly | Ala | Pro | Phe | Gly | Gly | Tyr | Lys | Lys | Ser | Gly | Ile | Gly | Arg | |
| 55 | | 465 | | | | 470 | | | | | 475 | | | | | 480 | |

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
 1 5 10 15
 Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
 20 25 30
 Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
 35 40 45
 Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
 50 55 60
 Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
 65 70 75 80
 Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
 85 90 95
 Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
 100 105 110
 Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
 115 120 125
 Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
 130 135 140
 Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
 145 150 155 160
 Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
 165 170 175
 Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
 180 185 190
 Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
 195 200 205

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Pro | Ala | Ile | Ser | Thr | Asp | Glu | Asn | Arg | Gln | Asp | Pro | Thr | Val | Thr | Val | |
| | 210 | | | | | | 215 | | | | | 220 | | | | | |
| 5 | Thr | Asp | Lys | Val | Asn | Gly | Tyr | Ser | Leu | Ile | Asn | Asn | Gly | Lys | Ile | Gly | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| | Phe | Val | Asn | Ser | Glu | Leu | Arg | Arg | Ser | Asp | Met | Phe | Asp | Lys | Asn | Asn | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 10 | Pro | Gln | Asn | Tyr | Gln | Ala | Lys | Gly | Asn | Val | Ala | Ala | Leu | Gly | Arg | Val | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Asn | Ala | Asn | Asp | Ser | Thr | Asp | His | Gly | Asn | Phe | Asn | Gly | Ile | Ser | Lys | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 15 | Thr | Val | Asn | Val | Lys | Pro | Asp | Ser | Glu | Leu | Ile | Ile | Asn | Phe | Thr | Thr | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | Met | Gln | Thr | Asn | Ser | Lys | Gln | Gly | Ala | Thr | Asn | Leu | Val | Ile | Lys | Asp | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 20 | Ala | Lys | Lys | Asn | Thr | Glu | Leu | Ala | Thr | Val | Asn | Val | Ala | Lys | Thr | Gly | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| | Thr | Ala | His | Leu | Phe | Lys | Val | Pro | Thr | Asp | Ala | Asp | Arg | Leu | Asp | Leu | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| 25 | Gln | Phe | Ile | Pro | Asp | Asn | Thr | Ala | Val | Ala | Asp | Ala | Ser | Arg | Ile | Thr | |
| | | | 355 | | | | | 360 | | | | | 365 | | | | |
| | Thr | Asn | Lys | Asp | Gly | Tyr | Lys | Tyr | Tyr | Ser | Phe | Ile | Asp | Asn | Val | Gly | |
| 30 | | 370 | | | | | 375 | | | | | 380 | | | | | |
| | Leu | Phe | Ser | Gly | Ser | His | Leu | Tyr | Val | Lys | Asn | Arg | Asp | Leu | Ala | Pro | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| | Lys | Ala | Thr | Asn | Asn | Lys | Glu | Tyr | Thr | Ile | Asn | Thr | Glu | Ile | Gly | Asn | |
| 35 | | | | | 405 | | | | | 410 | | | | | 415 | | |
| | Asn | Gly | Asn | Phe | Gly | Ala | Ser | Leu | Lys | Ala | Asp | Gln | Phe | Lys | Tyr | Glu | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | |
| 40 | Val | Thr | Leu | Pro | Gln | Gly | Val | Thr | Tyr | Val | Asn | Asn | Ser | Leu | Thr | Thr | |
| | | | 435 | | | | | 440 | | | | | 445 | | | | |
| | Thr | Phe | Pro | Asn | Gly | Asn | Glu | Asp | Ser | Thr | Val | Leu | Lys | Asn | Met | Thr | |
| | | 450 | | | | | 455 | | | | | 460 | | | | | |
| 45 | Val | Asn | Tyr | Asp | Gln | Asn | Ala | Asn | Lys | Val | Thr | Phe | Thr | Ser | Gln | Gly | |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| | Val | Thr | Thr | Ala | Arg | Gly | Thr | His | Thr | Lys | Glu | Val | Leu | Phe | Pro | Asp | |
| | | | | | 485 | | | | | 490 | | | | | 495 | | |
| 50 | Lys | Ser | Leu | Lys | Leu | Ser | Tyr | Lys | Val | Asn | Val | Ala | Asn | Ile | Asp | Thr | |
| | | | | 500 | | | | | 505 | | | | | 510 | | | |
| | Pro | Lys | Asn | Ile | Asp | Phe | Asn | Glu | Lys | Leu | Thr | Tyr | Arg | Thr | Ala | Ser | |
| 55 | | | 515 | | | | | 520 | | | | | 525 | | | | |

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
 1 5 10 15
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
 20 25 30
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
 25 35 40 45
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
 50 55 60
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe
 30 65 70 75 80
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
 85 90 95
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
 35 100 105 110
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
 115 120 125
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
 40 130 135 140
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
 145 150 155 160
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
 45 165 170 175
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
 180 185 190
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
 195 200 205
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
 55 210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
165 170 175

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Ala | Ile | Leu | Thr | Thr | Asp | Thr | Cys | Thr | Lys | His | Ile | Ala | Val | Ser | Leu |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| 5 | Lys | Ile | Asp | Gly | Lys | Thr | Val | Thr | Ile | Gly | Gly | Ser | Thr | Lys | Gly | Ser |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| | Gly | Met | Ile | His | Pro | Asn | Met | Ala | Thr | Met | Leu | Ala | Phe | Ile | Thr | Thr |
| | | 210 | | | | | 215 | | | | | 220 | | | | |
| 10 | Asp | Ala | Ser | Ile | Glu | Ser | Asn | Thr | Leu | His | Gln | Leu | Leu | Lys | Ser | Ser |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| | Thr | Asp | His | Thr | Phe | Asn | Met | Ile | Thr | Val | Asp | Gly | Asp | Thr | Ser | Thr |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| 15 | Asn | Asp | Met | Val | Leu | Val | Met | Ala | Asn | His | Gln | Val | Glu | His | Gln | Ile |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| | Leu | Ser | Gln | Asp | His | Pro | Gln | Trp | Glu | Thr | Phe | Val | Asp | Ala | Phe | Asn |
| 20 | | | 275 | | | | | 280 | | | | | 285 | | | |
| | Phe | Val | Cys | Thr | Phe | Leu | Ala | Lys | Ala | Ile | Ala | Arg | Asp | Gly | Glu | Gly |
| | | 290 | | | | | 295 | | | | | 300 | | | | |
| 25 | Ala | Thr | Lys | Leu | Ile | Ser | Val | Asn | Val | Ser | Gly | Ala | Lys | Ser | Ile | Ser |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| | Asp | Ala | Arg | Lys | Ile | Gly | Lys | Thr | Ile | Val | Ser | Ser | Asn | Leu | Val | Lys |
| | | | | | 325 | | | | | 330 | | | | | 335 | |
| 30 | Ser | Ala | Ile | Phe | Gly | Glu | Asp | Ala | Asn | Phe | Gly | Arg | Ile | Ile | Thr | Ala |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| | Ile | Gly | Tyr | Ser | Gly | Cys | Glu | Ile | Asp | Pro | Asn | Cys | Thr | Tyr | Val | Gln |
| 35 | | | 355 | | | | | 360 | | | | | 365 | | | |
| | Leu | Asn | Gln | Ile | Pro | Val | Val | Asp | Lys | Gly | Met | Ala | Val | Leu | Phe | Asp |
| | | 370 | | | | | 375 | | | | | 380 | | | | |
| 40 | Glu | Gln | Ala | Met | Ser | Asn | Thr | Leu | Thr | His | Glu | Asn | Val | Thr | Ile | Asp |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| | Val | Gln | Leu | Gly | Leu | Gly | Asn | Ala | Ala | Ala | Thr | Ala | Tyr | Gly | Cys | Asp |
| | | | | | 405 | | | | 410 | | | | | | 415 | |
| 45 | Leu | Ser | Tyr | Asp | Tyr | Val | Arg | Ile | Asn | Ala | Ser | Tyr | Arg | Thr | | |
| | | | | 420 | | | | | 425 | | | | | 430 | | |

(2) INFORMATION FOR SEQ ID NO:5245:

- | | |
|----|-------------------------------|
| 50 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 469 amino acids |
| | (B) TYPE: amino acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 55 | (ii) MOLECULE TYPE: protein |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

| | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5 | Asn | Pro | Ala | Leu | Thr | Val | Phe | Ala | Phe | Ile | Met | Ile | Ile | Ser | Ile | Leu | 1 | 5 | 10 | 15 |
| | Leu | Ala | Tyr | Val | Phe | Lys | Trp | Leu | Gly | Leu | Val | Asp | Asp | Val | Leu | Leu | 20 | 25 | 30 | |
| 10 | Met | Val | Ile | Ile | Ile | Ser | Thr | Ile | Ser | Leu | Gly | Val | Val | Val | Pro | Thr | 35 | 40 | 45 | |
| | Leu | Lys | Glu | Met | Asn | Ile | Met | Arg | Thr | Thr | Ile | Gly | Gln | Phe | Ile | Leu | 50 | 55 | 60 | |
| 15 | Leu | Val | Ala | Val | Leu | Ala | Asp | Leu | Val | Thr | Met | Ile | Leu | Leu | Thr | Val | 65 | 70 | 75 | 80 |
| | Tyr | Gly | Ala | Ile | Asn | Gly | Gln | Gly | Gly | Ser | Thr | Ile | Trp | Leu | Ile | Gly | 85 | 90 | 95 | |
| 20 | Ile | Leu | Val | Val | Phe | Thr | Ala | Ile | Ser | Tyr | Ile | Leu | Gly | Val | Gln | Phe | 100 | 105 | 110 | |
| | Lys | Arg | Met | Ser | Phe | Leu | Gln | Lys | Leu | Met | Asp | Gly | Thr | Thr | Gln | Ile | 115 | 120 | 125 | |
| 25 | Gly | Ile | Arg | Ala | Val | Phe | Ala | Leu | Ile | Ile | Leu | Leu | Val | Ala | Leu | Ala | 130 | 135 | 140 | |
| | Glu | Gly | Val | Gly | Ala | Glu | Asn | Ile | Leu | Gly | Ala | Phe | Leu | Ala | Gly | Val | 145 | 150 | 155 | 160 |
| 30 | Val | Val | Ser | Leu | Leu | Asn | Pro | Asp | Glu | Glu | Met | Val | Glu | Lys | Leu | Asp | 165 | 170 | 175 | |
| | Ser | Phe | Gly | Tyr | Gly | Phe | Phe | Ile | Pro | Ile | Phe | Phe | Ile | Met | Xaa | Gly | 180 | 185 | 190 | |
| | Val | Asp | Leu | Asn | Ile | Pro | Ser | Leu | Ile | Lys | Glu | Pro | Lys | Leu | Leu | Ile | 195 | 200 | 205 | |
| 40 | Ile | Ile | Pro | Ile | Leu | Ile | Val | Ala | Phe | Ile | Ile | Ser | Lys | Leu | Ile | Pro | 210 | 215 | 220 | |
| | Val | Met | Phe | Ile | Arg | Arg | Trp | Phe | Asp | Met | Lys | Thr | Thr | Ile | Ala | Ser | 225 | 230 | 235 | 240 |
| 45 | Ala | Phe | Leu | Leu | Thr | Ser | Thr | Leu | Ser | Leu | Val | Ile | Ala | Ala | Ala | Lys | 245 | 250 | 255 | |
| | Ile | Ser | Glu | Arg | Leu | Asn | Ala | Ile | Ser | Ala | Glu | Thr | Ser | Gly | Ile | Leu | 260 | 265 | 270 | |
| 50 | Ile | Leu | Ser | Ala | Val | Ile | Thr | Cys | Val | Phe | Val | Pro | Ile | Ile | Phe | Lys | 275 | 280 | 285 | |
| 55 | Lys | Leu | Phe | Pro | Val | Pro | Asp | Glu | Phe | Asn | Arg | Lys | Ile | Glu | Val | Ser | 290 | 295 | 300 | |

Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr
 305 310 315 320
 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp
 5 325 330 335
 Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr
 340 345 350
 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
 10 355 360 365
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
 370 375 380
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
 15 385 390 395 400
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
 20 405 410 415
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
 420 425 430
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
 25 435 440 445
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
 450 455 460
 Gly Gly Asp Ile Ile
 30 465

(2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 414 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
 1 5 10 15
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
 50 20 25 30
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
 35 40 45
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
 55 50 55 60

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Asn | Ile | Tyr | Arg | Arg | Leu | Thr | Asp | Ser | Glu | Glu | Gln | Leu | Lys | Gly | Glu | |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| 5 | Asn | Leu | Ile | Ile | Ser | Ala | Thr | Thr | Glu | Val | Phe | Lys | Pro | Ile | Met | Ser | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| | Ser | Thr | Leu | Val | Thr | Ile | Ile | Val | Phe | Leu | Pro | Leu | Val | Phe | Val | Ser | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| 10 | Gly | Ser | Val | Gly | Glu | Met | Phe | Arg | Pro | Phe | Ala | Leu | Ala | Ile | Ala | Phe | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| | Ser | Leu | Leu | Ala | Ser | Leu | Leu | Val | Ser | Ile | Thr | Leu | Val | Pro | Ala | Leu | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 15 | Ala | Ala | Thr | Leu | Phe | Lys | Lys | Gly | Val | Lys | Arg | Arg | Asn | Lys | Gln | His | |
| | 145 | | | | | 150 | | | | | 155 | | | | 160 | | |
| | Gln | Glu | Gly | Leu | Gly | Val | Val | Ser | Thr | Thr | Tyr | Lys | Lys | Val | Leu | His | |
| | | | | 165 | | | | | | 170 | | | | | 175 | | |
| 20 | Trp | Ser | Leu | Asn | His | Lys | Trp | Ile | Val | Ile | Ile | Leu | Ser | Thr | Leu | Ile | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Leu | Val | Ala | Thr | Ile | Val | Phe | Gly | Gly | Pro | Arg | Leu | Gly | Thr | Ser | Phe | |
| 25 | | | 195 | | | | | 200 | | | | 205 | | | | | |
| | Ile | Ser | Ala | Gly | Asp | Asp | Lys | Phe | Leu | Ala | Ile | Thr | Tyr | Thr | Pro | Lys | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 30 | Pro | Gly | Glu | Thr | Glu | Gln | Ala | Val | Leu | Asn | His | Ala | Lys | Asp | Val | Glu | |
| | 225 | | | | | 230 | | | | | 235 | | | | 240 | | |
| | Lys | Tyr | Leu | Lys | Gln | Lys | Lys | His | Val | Lys | Thr | Ile | Gln | Tyr | Ser | Val | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| 35 | Gly | Gly | Ser | Ser | Pro | Val | Asp | Pro | Thr | Gly | Ser | Thr | Asn | Ser | Met | Ala | |
| | | | | 260 | | | | 265 | | | | | | 270 | | | |
| | Ile | Met | Val | Glu | Tyr | Asp | Asn | Asp | Thr | Pro | Asn | Phe | Asp | Val | Glu | Ala | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| 40 | Asp | Lys | Val | Ile | Lys | His | Ala | Asp | Gly | Phe | Lys | His | Pro | Gly | Glu | Trp | |
| | 290 | | | | | | 295 | | | | | 300 | | | | | |
| | Lys | Asn | Gln | Asp | Leu | Gly | Thr | Gly | Ala | Gly | Asn | Lys | Ser | Val | Glu | Val | |
| 45 | 305 | | | | | 310 | | | | 315 | | | | | 320 | | |
| | Thr | Val | Lys | Gly | Pro | Ser | Met | Asp | Ala | Ile | Lys | Ser | Thr | Val | Lys | Asp | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| | Ile | Glu | Gln | Lys | Met | Lys | Gln | Val | Lys | Gly | Leu | Ala | Asn | Val | Lys | Ser | |
| 50 | | | | 340 | | | | 345 | | | | | 350 | | | | |
| | Asp | Leu | Ser | Gln | Thr | Tyr | Asp | Gln | Tyr | Glu | Ile | Lys | Val | Asp | Gln | Asn | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| 55 | Lys | Ala | Ala | Glu | Asn | Gly | Ile | Ser | Ala | Ser | Gln | Leu | Ala | Met | His | Leu | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
 385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
 1 5 10 15

Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
 20 25 30

Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
 35 40 45

Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
 50 55 60

Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Arg Ala Thr Val
 65 70 75 80

Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
 85 90 95

His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
 100 105 110

Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
 115 120 125

Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
 130 135 140

Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
 145 150 155 160

Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
 165 170 175

Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
 180 185 190

Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
 195 200 205

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Lys | Leu | Phe | Asn | Arg | Thr | Glu | Gln | Thr | Glu | Lys | His | Ile | Tyr | Asp | Asp | |
| | 210 | | | | | | 215 | | | | | 220 | | | | | |
| 5 | Ser | Thr | Gln | Phe | Arg | Thr | Leu | Thr | Met | Arg | Ile | Leu | Arg | Ser | Ala | Phe | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| | Leu | Ser | Gly | Leu | Met | Leu | Glu | Phe | Ile | Ser | Met | Leu | Gly | Ile | Gly | Leu | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 10 | Val | Ala | Leu | Glu | Ala | Thr | Leu | Ser | Leu | Val | Val | Phe | His | Asn | Ile | Asp | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Phe | Lys | Thr | Ala | Ala | Ile | Ala | Ile | Ile | Leu | Ala | Pro | Glu | Phe | Tyr | Asn | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 15 | Ala | Ile | Lys | Asp | Leu | Gly | Gln | Ala | Phe | His | Thr | Gly | Lys | Gln | Ser | Glu | |
| | 290 | | | | | 295 | | | | | | 300 | | | | | |
| | Gly | Ala | Ser | Asp | Val | Val | Phe | Glu | Phe | Leu | Glu | Gln | Pro | Asn | Tyr | Asn | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 20 | Asn | Glu | Phe | Leu | Leu | Lys | Tyr | Glu | Glu | Asn | Gln | Lys | Pro | Phe | Ile | Gln | |
| | | | | 325 | | | | | | 330 | | | | | 335 | | |
| | Leu | Thr | Asp | Ile | Ser | Phe | Arg | Tyr | Asp | Asp | Ser | Asp | Arg | Leu | Val | Leu | |
| | | | 340 | | | | | | 345 | | | | | 350 | | | |
| 25 | Asn | Asp | Leu | Asn | Leu | Glu | Ile | Phe | Lys | Gly | Asp | Gln | Ile | Ala | Leu | Val | |
| | | | 355 | | | | | 360 | | | | | 365 | | | | |
| | Gly | Pro | Ser | Gly | Ala | Gly | Lys | Ser | Thr | Leu | Thr | His | Leu | Ile | Ala | Gly | |
| 30 | | 370 | | | | 375 | | | | | | 380 | | | | | |
| | Val | Tyr | Gln | Pro | Thr | Ile | Gly | Thr | Ile | Ser | Thr | Asn | Gln | Arg | Asp | Leu | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| | Asn | Ile | Gly | Ile | Leu | Ser | Gln | Gln | Pro | Tyr | Ile | Phe | Ser | Ala | Ser | Ile | |
| 35 | | | | | 405 | | | | | 410 | | | | | 415 | | |
| | Lys | Glu | Asn | Ile | Thr | Met | Phe | Lys | Asp | Ile | Glu | Asn | Asn | Thr | Ile | Glu | |
| | | | 420 | | | | | | 425 | | | | | 430 | | | |
| 40 | Glu | Val | Leu | Asp | Glu | Val | Gly | Leu | Leu | Asp | Lys | Val | Gln | Ser | Phe | Thr | |
| | | 435 | | | | | 440 | | | | | | 445 | | | | |
| | Lys | Gly | Ile | Asn | Thr | Ile | Ile | Gly | Glu | Gly | Gly | Glu | Met | Leu | Ser | Gly | |
| | | 450 | | | | | 455 | | | | | 460 | | | | | |
| 45 | Gly | Gln | Met | Arg | Arg | Ile | Glu | Leu | Cys | Arg | Leu | Leu | Val | Met | Lys | Pro | |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| | Asp | Leu | Val | Ile | Phe | Asp | Glu | Pro | Ala | Thr | Gly | Leu | Asp | Ile | Gln | Thr | |
| | | | | 485 | | | | | | 490 | | | | | 495 | | |
| 50 | Glu | His | Met | Ile | Gln | Asn | Val | Leu | Phe | Gln | His | Phe | Lys | Asp | Thr | Thr | |
| | | | 500 | | | | | | 505 | | | | | 510 | | | |
| | Met | Ile | Val | Ile | Ala | His | Arg | Asp | Asn | Thr | Ile | Arg | His | Leu | Gln | Arg | |
| 55 | | | 515 | | | | | 520 | | | | | 525 | | | | |

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
530 535 540

5 Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

20

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
1 5 10 15

25

Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
20 25 30

Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
35 40 45

30

Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr
50 55 60

Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
65 70 75 80

35

Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
85 90 95

Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
100 105 110

40

Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
115 120 125

Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
130 135 140

45

Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
145 150 155 160

Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
165 170 175

50

Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
180 185 190

55

Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp
195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala
275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn
340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn
370 375 380

30 Gln Ile Asn Gln Ile Met Gln Tyr Lys
385 390

(2) INFORMATION FOR SEQ ID NO:5249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
20 25 30

55 Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala
35 40 45

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Ser | Glu | Asn | Ser | Val | Thr | Gln | Ser | Asp | Ser | Ala | Ser | Asn | Glu | Ser | Lys |
| | 50 | | | | | | 55 | | | | | 60 | | | | |
| 5 | Ser | Asn | Asp | Ser | Ser | Ser | Val | Ser | Ala | Ala | Pro | Lys | Thr | Asp | Asp | Thr |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| | Asn | Val | Ser | Asp | Thr | Lys | Thr | Ser | Ser | Asn | Thr | Asn | Asn | Gly | Glu | Thr |
| | | | | | 85 | | | | | 90 | | | | | 95 | |
| 10 | Ser | Val | Ala | Gln | Asn | Pro | Ala | Gln | Gln | Glu | Thr | Thr | Gln | Ser | Ser | Ser |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| | Thr | Asn | Ala | Thr | Thr | Glu | Glu | Thr | Pro | Val | Thr | Gly | Glu | Ala | Thr | Thr |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| 15 | Thr | Thr | Thr | Asn | Gln | Ala | Asn | Thr | Pro | Ala | Thr | Thr | Gln | Ser | Ser | Asn |
| | | 130 | | | | | 135 | | | | | 140 | | | | |
| | Thr | Asn | Ala | Glu | Glu | Leu | Val | Asn | Gln | Thr | Ser | Asn | Glu | Thr | Thr | Ser |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| 20 | Asn | Asp | Thr | Asn | Thr | Val | Ser | Ser | Val | Asn | Ser | Pro | Gln | Asn | Ser | Thr |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| | Asn | Ala | Glu | Asn | Val | Ser | Thr | Thr | Gln | Asp | Thr | Ser | Thr | Glu | Ala | Thr |
| 25 | | | | 180 | | | | | 185 | | | | | 190 | | |
| | Pro | Ser | Asn | Asn | Glu | Ser | Ala | Pro | Gln | Ser | Thr | Asp | Ala | Ser | Asn | Lys |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| 30 | Asp | Val | Val | Asn | Gln | Ala | Val | Asn | Thr | Ser | Ala | Pro | Arg | Met | Arg | Ala |
| | 210 | | | | | 215 | | | | | | 220 | | | | |
| | Phe | Ser | Leu | Ala | Ala | Val | Ala | Ala | Asp | Ala | Pro | Val | Ala | Gly | Thr | Asp |
| | 225 | | | | | 230 | | | | 235 | | | | | | 240 |
| 35 | Ile | Thr | Asn | Gln | Leu | Thr | Asn | Val | Thr | Val | Gly | Ile | Asp | Ser | Gly | Thr |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| | Thr | Val | Tyr | Pro | His | Gln | Ala | Gly | Tyr | Val | Lys | Leu | Asn | Tyr | Gly | Phe |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| 40 | Ser | Val | Pro | Asn | Ser | Ala | Val | Lys | Gly | Asp | Thr | Phe | Lys | Ile | Thr | Val |
| | | | 275 | | | | | 280 | | | | | 285 | | | |
| | Pro | Lys | Glu | Leu | Asn | Leu | Asn | Gly | Val | Thr | Ser | Thr | Ala | Lys | Val | Pro |
| | | 290 | | | | 295 | | | | | | 300 | | | | |
| 45 | Pro | Ile | Met | Ala | Gly | Asp | Gln | Val | Leu | Ala | Asn | Gly | Val | Ile | Asp | Ser |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| | Asp | Gly | Asn | Val | Ile | Tyr | Thr | Phe | Thr | Asp | Tyr | Val | Asn | Thr | Lys | Asp |
| 50 | | | | | 325 | | | | | 330 | | | | | 335 | |
| | Asp | Val | Lys | Ala | Thr | Leu | Thr | Met | Pro | Ala | Tyr | Ile | Asp | Pro | Glu | Asn |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| 55 | Val | Lys | Lys | Thr | Gly | Asn | Val | Thr | Leu | Ala | Thr | Gly | Ile | Gly | Ser | Thr |
| | | | 355 | | | | | 360 | | | | | 365 | | | |

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Thr | Ala | Asn | Lys | Thr | Val | Leu | Val | Asp | Tyr | Glu | Lys | Tyr | Gly | Lys | Phe |
| | 370 | | | | | | 375 | | | | | 380 | | | | |
| 5 | Tyr | Asn | Leu | Ser | Ile | Lys | Gly | Thr | Ile | Asp | Gln | Ile | Asp | Lys | Thr | Asn |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| | Asn | Thr | Tyr | Arg | Gln | Thr | Ile | Tyr | Val | Asn | Pro | Ser | Gly | Asp | Asn | Val |
| | | | | | 405 | | | | | 410 | | | | | 415 | |
| 10 | Ile | Ala | Pro | Val | Leu | Thr | Gly | Asn | Leu | Lys | Pro | Asn | Thr | Asp | Ser | Asn |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| | Ala | Leu | Ile | Asp | Gln | Gln | Asn | Thr | Ser | Ile | Lys | Val | Tyr | Lys | Val | Asp |
| | | | 435 | | | | | 440 | | | | | 445 | | | |
| 15 | Asn | Ala | Ala | Asp | Leu | Ser | Glu | Ser | Tyr | Phe | Val | Asn | Pro | Glu | Asn | Phe |
| | 450 | | | | | | 455 | | | | | 460 | | | | |
| | Glu | Asp | Val | Thr | Asn | Ser | Val | Asn | Ile | Thr | Phe | Pro | Asn | Pro | Asn | Gln |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| 20 | Tyr | Lys | Val | Glu | Phe | Asn | Thr | Pro | Asp | Asp | Gln | Ile | Thr | Thr | Pro | Tyr |
| | | | | | 485 | | | | | 490 | | | | | 495 | |
| | Ile | Val | Val | Val | Asn | Gly | His | Ile | Asp | Pro | Asn | Ser | Lys | Gly | Asp | Leu |
| 25 | | | | 500 | | | | | 505 | | | | | 510 | | |
| | Ala | Leu | Arg | Ser | Thr | Leu | Tyr | Gly | Tyr | Asn | Ser | Asn | Ile | Ile | Trp | Arg |
| | | | 515 | | | | | 520 | | | | | 525 | | | |
| 30 | Ser | Met | Ser | Trp | Asp | Asn | Glu | Val | Ala | Phe | Asn | Asn | Gly | Ser | Gly | Ser |
| | 530 | | | | | | 535 | | | | | | 540 | | | |
| | Gly | Asp | Gly | Ile | Asp | Lys | Pro | Val | Val | Pro | Glu | Gln | Pro | Asp | Glu | Pro |
| | 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| 35 | Gly | Glu | Ile | Glu | Pro | Ile | Pro | Glu | Asp | Ser | Asp | Ser | Asp | Pro | Gly | Ser |
| | | | | | 565 | | | | | 570 | | | | | 575 | |
| | Asp | Ser | Gly | Ser | Asp | Ser | Asn | Ser | Asp | Ser | Gly | Ser | Asp | Ser | Gly | Ser |
| | | | | 580 | | | | | 585 | | | | | 590 | | |
| 40 | Asp | Ser | Thr | Ser | Asp | Ser | Gly | Ser | Asp | Ser | Ala | Ser | Asp | Ser | Asp | Ser |
| | | | 595 | | | | | 600 | | | | | 605 | | | |
| | Ala | Ser | Asp | Ser | Asp | Ser | Ala | Ser | Asp | Ser | Asp | Ser | Ala | Ser | Asp | Ser |
| | | | 610 | | | | 615 | | | | | 620 | | | | |
| 45 | Asp | Ser | Ala | Ser | Asp | Ser | Asp | Ser | Asp | Asn | Asp | Ser | Asp | Ser | Asp | Ser |
| | 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | | 645 | | | | | | 650 | | | | | 655 | |
| 50 | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | | 660 | | | | | 665 | | | | | 670 | | |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| 55 | | | 675 | | | | 680 | | | | | 685 | | | | |

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | 690 | | | | | 695 | | | | | 700 | | | | | |
| 5 | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | | | 725 | | | | | 730 | | | | | 735 | |
| 10 | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | | 740 | | | | | 745 | | | | | 750 | | |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | 755 | | | | 760 | | | | | 765 | | | | |
| 15 | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Ala | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | 770 | | | | | | 775 | | | | | 780 | | | | |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| 20 | 785 | | | | | 790 | | | | | 795 | | | | | 800 |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | | | 805 | | | | | 810 | | | | | | 815 |
| 25 | Glu | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser |
| | | | | 820 | | | | | 825 | | | | | | 830 | |
| | Asp | Ser | Asp | Ser | Asp | Ser | Asp | Ser | Ala | Ser | Asp | Ser | Asp | Ser | Gly | Ser |
| | | | 835 | | | | | 840 | | | | | 845 | | | |
| 30 | Asp | Ser | Asp | Ser | Ser | Ser | Asp | Ser | Asp | Ser | Glu | Ser | Asp | Ser | Asn | Ser |
| | 850 | | | | | | 855 | | | | | 860 | | | | |
| | Asp | Ser | Glu | Ser | Val | Ser | Asn | Asn | Asn | Val | Val | Pro | Pro | Asn | Ser | Pro |
| 35 | 865 | | | | | 870 | | | | | 875 | | | | | 880 |
| | Lys | Asn | Gly | Thr | Asn | Ala | Ser | Asn | Lys | Asn | Glu | Ala | Lys | Asp | Ser | Lys |
| | | | | | 885 | | | | | 890 | | | | | 895 | |
| 40 | Glu | Pro | Leu | Pro | Asp | Thr | Gly | Ser | Glu | Asp | Glu | Ala | Asn | Thr | Ser | Leu |
| | | | | 900 | | | | | 905 | | | | | 910 | | |
| | Ile | Trp | Gly | Leu | Leu | Ala | Ser | Ile | Gly | Ser | Leu | Leu | Leu | Phe | Arg | Arg |
| | | | 915 | | | | | 920 | | | | | | 925 | | |
| 45 | Lys | Lys | Glu | Asn | Lys | Asp | Lys | Lys | | | | | | | | |
| | 930 | | | | | | 935 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5250:

- | | |
|----|-------------------------------|
| 50 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 194 amino acids |
| | (B) TYPE: amino acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 55 | (ii) MOLECULE TYPE: protein |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala
 1 5 10 15
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro
 20 25 30
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu
 35 40 45
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys
 50 55 60
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys
 65 70 75 80
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
 85 90 95
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
 100 105 110
 Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
 115 120 125
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
 130 135 140
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
 145 150 155 160
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
 165 170 175
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
 180 185 190
 Ile Leu

(2) INFORMATION FOR SEQ ID NO:5251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55 Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
 1 5 10 15

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Val | Thr | Asp | Asn | Met | Ser | Leu | Asp | Phe | Asp | Thr | Asn | Gly | Gly | Tyr | Ser | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| 5 | Leu | Asn | Phe | Asn | Asn | Leu | Asp | Gln | Ser | Lys | Asn | Tyr | Val | Ile | Lys | Tyr | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| | Glu | Gly | Tyr | Tyr | Asp | Ser | Asn | Ala | Ser | Asn | Leu | Glu | Phe | Gln | Thr | His | |
| | | 50 | | | | | 55 | | | | | 60 | | | | | |
| 10 | Leu | Phe | Gly | Tyr | Tyr | Asn | Tyr | Tyr | Tyr | Thr | Ser | Asn | Leu | Thr | Trp | Lys | |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| | Asn | Gly | Val | Ala | Phe | Tyr | Ser | Asn | Asn | Ala | Gln | Gly | Asp | Gly | Lys | Asp | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 15 | Lys | Leu | Lys | Glu | Pro | Ile | Ile | Glu | His | Ser | Thr | Pro | Ile | Glu | Leu | Glu | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Phe | Lys | Ser | Glu | Pro | Pro | Val | Glu | Lys | His | Glu | Leu | Thr | Gly | Thr | Ile | |
| 20 | | | 115 | | | | | 120 | | | | | 125 | | | | |
| | Glu | Glu | Ser | Asn | Asp | Ser | Lys | Pro | Ile | Asp | Phe | Glu | Tyr | His | Thr | Ala | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 25 | Val | Glu | Gly | Ala | Glu | Gly | His | Ala | Glu | Gly | Thr | Ile | Glu | Thr | Glu | Glu | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| | Asp | Ser | Ile | His | Val | Asp | Phe | Glu | Glu | Ser | Thr | His | Glu | Asn | Ser | Lys | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 30 | His | His | Ala | Asp | Val | Val | Glu | Tyr | Glu | Glu | Asp | Thr | Asn | Pro | Gly | Gly | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Gly | Gln | Val | Thr | Thr | Glu | Ser | Asn | Leu | Val | Glu | Phe | Asp | Glu | Asp | Ser | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 35 | Thr | Lys | Gly | Ile | Val | Thr | Gly | Ala | Val | Ser | Asp | His | Thr | Thr | Ile | Glu | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Asp | Thr | Lys | Glu | Tyr | Thr | Thr | Glu | Ser | Asn | Leu | Ile | Glu | Leu | Val | Asp | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 40 | Glu | Leu | Pro | Glu | Glu | His | Gly | Gln | Ala | Gln | Gly | Pro | Ile | Glu | Glu | Ile | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| | Thr | Glu | Asn | Asn | His | His | Ile | Ser | His | Ser | Gly | Leu | Gly | Thr | Glu | Asn | |
| 45 | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Gly | His | Gly | Asn | Tyr | Gly | Val | Ile | Glu | Glu | Ile | Glu | Glu | Asn | Ser | His | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 50 | Val | Asp | Ile | Lys | Ser | Glu | Leu | Gly | Tyr | Glu | Gly | Gly | Gln | Asn | Ser | Gly | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | Asn | Gln | Ser | Phe | Glu | Glu | Asp | Thr | Glu | Glu | Asp | Lys | Pro | Lys | Tyr | Glu | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 55 | Gln | Gly | Gly | Asn | Ile | Val | Asp | Ile | Asp | Phe | Asp | Ser | Val | Pro | Gln | Ile | |
| | | | | 325 | | | | | | 330 | | | | | 335 | | |

EP 0 786 519 A2

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
340 345 350

5 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
355 360 365

Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile
370 375 380

10 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
385 390 395 400

Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
405 410 415

15 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
420 425 430

Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro
435 440 445

20 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro
450 455 460

25 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala
465 470 475 480

Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val
485 490 495

30 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro
500 505 510

Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly
515 520 525

35 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile
530 535 540

Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala
545 550 555

40 (2) INFORMATION FOR SEQ ID NO:5252:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

55 Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu
1 5 10 15

EP 0 786 519 A2

Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
130 135 140

Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
145 150 155 160

25 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
165 170 175

Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
180 185 190

30 Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
195 200 205

Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
210 215 220

35 Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

EP 0 786 519 A2

1 Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 10 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 15 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 20 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
 25 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
 Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1027 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

1 Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
 50 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Lys | Thr | Ser | Glu | Thr | Gln | Thr | Thr | Ala | Thr | Asn | Val | Asn | His | Ile | Glu | 65 | 70 | 75 | 80 |
| 5 | Glu | Thr | Gln | Ser | Tyr | Asn | Ala | Thr | Val | Thr | Glu | Gln | Pro | Ser | Asn | Ala | 85 | 90 | 95 | |
| | Thr | Gln | Val | Thr | Thr | Glu | Glu | Ala | Pro | Lys | Ala | Val | Gln | Ala | Pro | Gln | 100 | 105 | 110 | |
| 10 | Thr | Ala | Gln | Pro | Ala | Asn | Ile | Glu | Thr | Val | Lys | Glu | Glu | Val | Val | Lys | 115 | 120 | 125 | |
| | Glu | Glu | Ala | Lys | Pro | Gln | Val | Lys | Glu | Thr | Thr | Gln | Ser | Gln | Asp | Asn | 130 | 135 | 140 | |
| 15 | Ser | Gly | Asp | Gln | Arg | Gln | Val | Asp | Leu | Thr | Pro | Lys | Lys | Ala | Thr | Gln | 145 | 150 | 155 | 160 |
| | Asn | Gln | Val | Ala | Glu | Thr | Gln | Val | Glu | Val | Ala | Gln | Pro | Arg | Thr | Ala | 165 | 170 | 175 | |
| 20 | Ser | Glu | Ser | Lys | Pro | Arg | Val | Thr | Arg | Ser | Ala | Asp | Val | Ala | Glu | Ala | 180 | 185 | 190 | |
| | Lys | Glu | Ala | Ser | Asn | Ala | Lys | Val | Glu | Thr | Gly | Thr | Asp | Val | Thr | Ser | 195 | 200 | 205 | |
| 25 | Lys | Val | Thr | Val | Glu | Ile | Gly | Ser | Ile | Glu | Gly | His | Asn | Asn | Thr | Asn | 210 | 215 | 220 | |
| | Lys | Val | Glu | Pro | His | Ala | Gly | Gln | Arg | Ala | Val | Leu | Lys | Tyr | Lys | Leu | 225 | 230 | 235 | 240 |
| | Lys | Phe | Glu | Asn | Gly | Leu | His | Gln | Gly | Asp | Tyr | Phe | Asp | Phe | Thr | Leu | 245 | 250 | 255 | |
| 35 | Ser | Asn | Asn | Val | Asn | Thr | His | Gly | Val | Ser | Thr | Ala | Arg | Lys | Val | Pro | 260 | 265 | 270 | |
| | Glu | Ile | Lys | Asn | Gly | Ser | Val | Val | Met | Ala | Thr | Gly | Glu | Val | Leu | Glu | 275 | 280 | 285 | |
| 40 | Gly | Gly | Lys | Ile | Arg | Tyr | Thr | Phe | Thr | Asn | Asp | Ile | Glu | Asp | Lys | Val | 290 | 295 | 300 | |
| | Asp | Val | Thr | Ala | Glu | Leu | Glu | Ile | Asn | Leu | Phe | Ile | Asp | Pro | Lys | Thr | 305 | 310 | 315 | 320 |
| 45 | Val | Gln | Thr | Asn | Gly | Asn | Gln | Thr | Ile | Thr | Ser | Thr | Leu | Asn | Glu | Glu | 325 | 330 | 335 | |
| | Gln | Thr | Ser | Lys | Glu | Leu | Asp | Val | Lys | Tyr | Lys | Asp | Gly | Ile | Gly | Asn | 340 | 345 | 350 | |
| 50 | Tyr | Tyr | Ala | Asn | Leu | Asn | Gly | Ser | Ile | Glu | Thr | Phe | Asn | Lys | Ala | Asn | 355 | 360 | 365 | |
| | Asn | Arg | Phe | Ser | His | Val | Ala | Phe | Ile | Lys | Pro | Asn | Asn | Gly | Lys | Thr | 370 | 375 | 380 | |

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Thr | Ser | Val | Thr | Val | Thr | Gly | Thr | Leu | Met | Lys | Gly | Ser | Asn | Gln | Asn | 385 | | 390 | | 395 | | 400 |
| 5 | Gly | Asn | Gln | Pro | Lys | Val | Arg | Ile | Phe | Glu | Tyr | Leu | Gly | Asn | Asn | Glu | | 405 | | 410 | | 415 | |
| | Asp | Ile | Ala | Lys | Ser | Val | Tyr | Ala | Asn | Thr | Thr | Asp | Thr | Ser | Lys | Phe | | 420 | | 425 | | 430 | |
| 10 | Lys | Glu | Val | Thr | Ser | Asn | Met | Ser | Gly | Asn | Leu | Asn | Leu | Gln | Asn | Asn | | 435 | | 440 | | 445 | |
| | Gly | Ser | Tyr | Ser | Leu | Asn | Ile | Glu | Asn | Leu | Asp | Lys | Thr | Tyr | Val | Val | | 450 | | 455 | | 460 | |
| 15 | His | Tyr | Asp | Gly | Glu | Tyr | Leu | Asn | Gly | Thr | Asp | Glu | Val | Asp | Phe | Arg | | 465 | | 470 | | 475 | 480 |
| | Thr | Gln | Met | Val | Gly | His | Pro | Glu | Gln | Leu | Tyr | Lys | Tyr | Tyr | Tyr | Asp | | 485 | | 490 | | 495 | |
| 20 | Arg | Gly | Tyr | Thr | Leu | Thr | Trp | Asp | Asn | Gly | Leu | Val | Leu | Tyr | Ser | Asn | | 500 | | 505 | | 510 | |
| | Lys | Ala | Asn | Gly | Asn | Glu | Lys | Asn | Gly | Pro | Ile | Ile | Gln | Asn | Asn | Lys | | 515 | | 520 | | 525 | |
| 25 | Phe | Glu | Tyr | Lys | Glu | Asp | Thr | Ile | Lys | Glu | Thr | Leu | Thr | Gly | Gln | Tyr | | 530 | | 535 | | 540 | |
| | Asp | Lys | Asn | Leu | Val | Thr | Thr | Val | Glu | Glu | Glu | Tyr | Asp | Ser | Ser | Thr | | 545 | | 550 | | 555 | 560 |
| | Leu | Asp | Ile | Asp | Tyr | His | Thr | Ala | Ile | Asp | Gly | Gly | Gly | Gly | Tyr | Val | | 565 | | 570 | | 575 | |
| 35 | Asp | Gly | Tyr | Ile | Glu | Thr | Ile | Glu | Glu | Thr | Asp | Ser | Ser | Ala | Ile | Asp | | 580 | | 585 | | 590 | |
| | Ile | Asp | Tyr | His | Thr | Ala | Val | Asp | Ser | Glu | Ala | Gly | His | Val | Gly | Gly | | 595 | | 600 | | 605 | |
| 40 | Tyr | Thr | Glu | Ser | Ser | Glu | Glu | Ser | Asn | Pro | Ile | Asp | Phe | Glu | Glu | Ser | | 610 | | 615 | | 620 | |
| | Thr | His | Glu | Asn | Ser | Lys | His | His | Ala | Asp | Val | Val | Glu | Tyr | Glu | Glu | | 625 | | 630 | | 635 | 640 |
| 45 | Asp | Thr | Asn | Pro | Gly | Gly | Gly | Gln | Val | Thr | Thr | Glu | Ser | Asn | Leu | Val | | 645 | | 650 | | 655 | |
| | Glu | Phe | Asp | Glu | Glu | Ser | Thr | Lys | Gly | Ile | Val | Thr | Gly | Ala | Val | Ser | | 660 | | 665 | | 670 | |
| 50 | Asp | His | Thr | Thr | Val | Glu | Asp | Thr | Lys | Glu | Tyr | Thr | Thr | Glu | Ser | Asn | | 675 | | 680 | | 685 | |
| | Leu | Ile | Glu | Leu | Val | Asp | Glu | Leu | Pro | Glu | Glu | His | Gly | Gln | Ala | Gln | | 690 | | 695 | | 700 | |

EP 0 786 519 A2

| | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|------|------|------|------|-----|
| | Gly | Pro | Val | Glu | Glu | Ile | Thr | Lys | Asn | Asn | His | His | Ile | Ser | His | Ser | 705 | | 710 | | 715 | | 720 |
| 5 | Gly | Leu | Gly | Thr | Glu | Asn | Gly | His | Gly | Asn | Tyr | Asp | Val | Ile | Glu | Glu | | 725 | | 730 | | 735 | |
| | Ile | Glu | Glu | Asn | Ser | His | Val | Asp | Ile | Lys | Ser | Glu | Leu | Gly | Tyr | Glu | | 740 | | 745 | | 750 | |
| 10 | Gly | Gly | Gln | Asn | Ser | Gly | Asn | Gln | Ser | Phe | Glu | Glu | Asp | Thr | Glu | Glu | | 755 | | 760 | | 765 | |
| | Asp | Lys | Pro | Lys | Tyr | Glu | Gln | Gly | Gly | Asn | Ile | Val | Asp | Ile | Asp | Phe | 770 | | 775 | | 780 | | |
| 15 | Asp | Ser | Val | Pro | Gln | Ile | His | Gly | Gln | Asn | Lys | Gly | Asn | Gln | Ser | Phe | 785 | | 790 | | 795 | | |
| | Glu | Glu | Asp | Thr | Glu | Lys | Asp | Lys | Pro | Lys | Tyr | Glu | His | Gly | Gly | Asn | | 805 | | 810 | | 815 | |
| 20 | Ile | Ile | Asp | Ile | Asp | Phe | Asp | Ser | Val | Pro | His | Ile | His | Gly | Phe | Asn | | 820 | | 825 | | 830 | |
| | Lys | His | Thr | Glu | Ile | Ile | Glu | Glu | Asp | Thr | Asn | Lys | Asp | Lys | Pro | Ser | | 835 | | 840 | | 845 | |
| 25 | Tyr | Gln | Phe | Gly | Gly | His | Asn | Ser | Val | Asp | Phe | Glu | Glu | Asp | Thr | Leu | 850 | | 855 | | 860 | | |
| | Pro | Lys | Val | Ser | Gly | Gln | Asn | Glu | Gly | Gln | Gln | Thr | Ile | Glu | Glu | Asp | 865 | | 870 | | 875 | | |
| 30 | Thr | Thr | Pro | Pro | Ile | Val | Pro | Pro | Thr | Pro | Pro | Thr | Pro | Glu | Val | Pro | | 885 | | 890 | | 895 | |
| | Ser | Glu | Pro | Glu | Thr | Pro | Thr | Pro | Pro | Thr | Pro | Glu | Val | Pro | Ser | Glu | | 900 | | 905 | | 910 | |
| 35 | Pro | Glu | Thr | Pro | Thr | Pro | Pro | Thr | Pro | Glu | Val | Pro | Ser | Glu | Pro | Glu | | 915 | | 920 | | 925 | |
| 40 | Thr | Pro | Thr | Pro | Pro | Thr | Pro | Glu | Val | Pro | Ala | Glu | Pro | Gly | Lys | Pro | 930 | | 935 | | 940 | | |
| | Val | Pro | Pro | Ala | Lys | Glu | Glu | Pro | Lys | Lys | Pro | Ser | Lys | Pro | Val | Glu | 945 | | 950 | | 955 | | |
| 45 | Gln | Gly | Lys | Val | Val | Thr | Pro | Val | Ile | Glu | Ile | Asn | Glu | Lys | Val | Lys | | 965 | | 970 | | 975 | |
| | Ala | Val | Ala | Pro | Thr | Lys | Lys | Pro | Gln | Ser | Lys | Lys | Ser | Glu | Leu | Pro | | 980 | | 985 | | 990 | |
| 50 | Glu | Thr | Gly | Gly | Glu | Glu | Ser | Thr | Asn | Lys | Gly | Met | Leu | Phe | Gly | Gly | | 995 | | 1000 | | 1005 | |
| | Leu | Phe | Ser | Ile | Leu | Gly | Leu | Ala | Leu | Leu | Arg | Arg | Asn | Lys | Lys | Asn | 1010 | | 1015 | | 1020 | | |
| 55 | | | | | | | | | | | | | | | | | | | | | | | |

His Lys Ala
1025

5 (2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

20 Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
1 5 10 15
Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
20 25 30
25 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys
35 40 45
Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp
50 55 60
30 Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu
65 70 75 80
Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val
35 85 90 95
Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
100 105 110
40 Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys
115 120 125
Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys
130 135 140
45 Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg
145 150 155

50 Claims

- 55 1. Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:

(a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;

(b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

(c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.

9. The nucleic acid fragment of claim 8 which is DNA.

10. The nucleic acid fragment of claim 8 which is RNA.

11. A vector comprising a fragment of claim 8.

12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably liked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

13. A vector comprising a fragment of claim 12.

14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.

15. A method for producing a polypeptide in a host cell comprising the steps of:

(a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and

(b) isolating said protein.

16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
 - (b) identifying members of said library which contain sequences that hybridize to said target sequence;
 - (c) isolating the nucleic acid molecules from said members identified in step (b).
19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) isolating mRNA, DNA, or cDNA produced from an organism;
 - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
 - (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8.
21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
 - (a) an isolated polypeptide antigen of claim 24, and
 - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

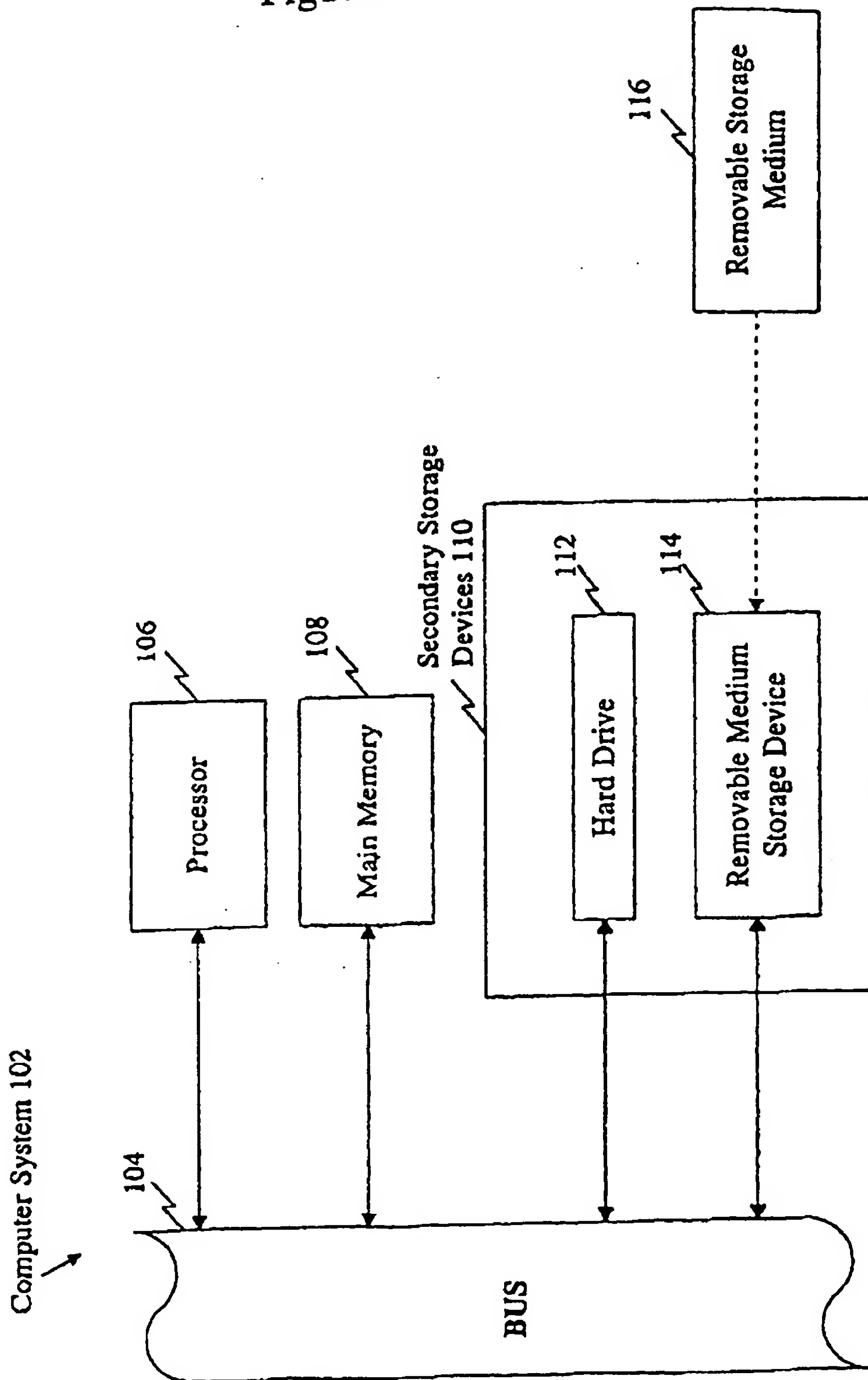
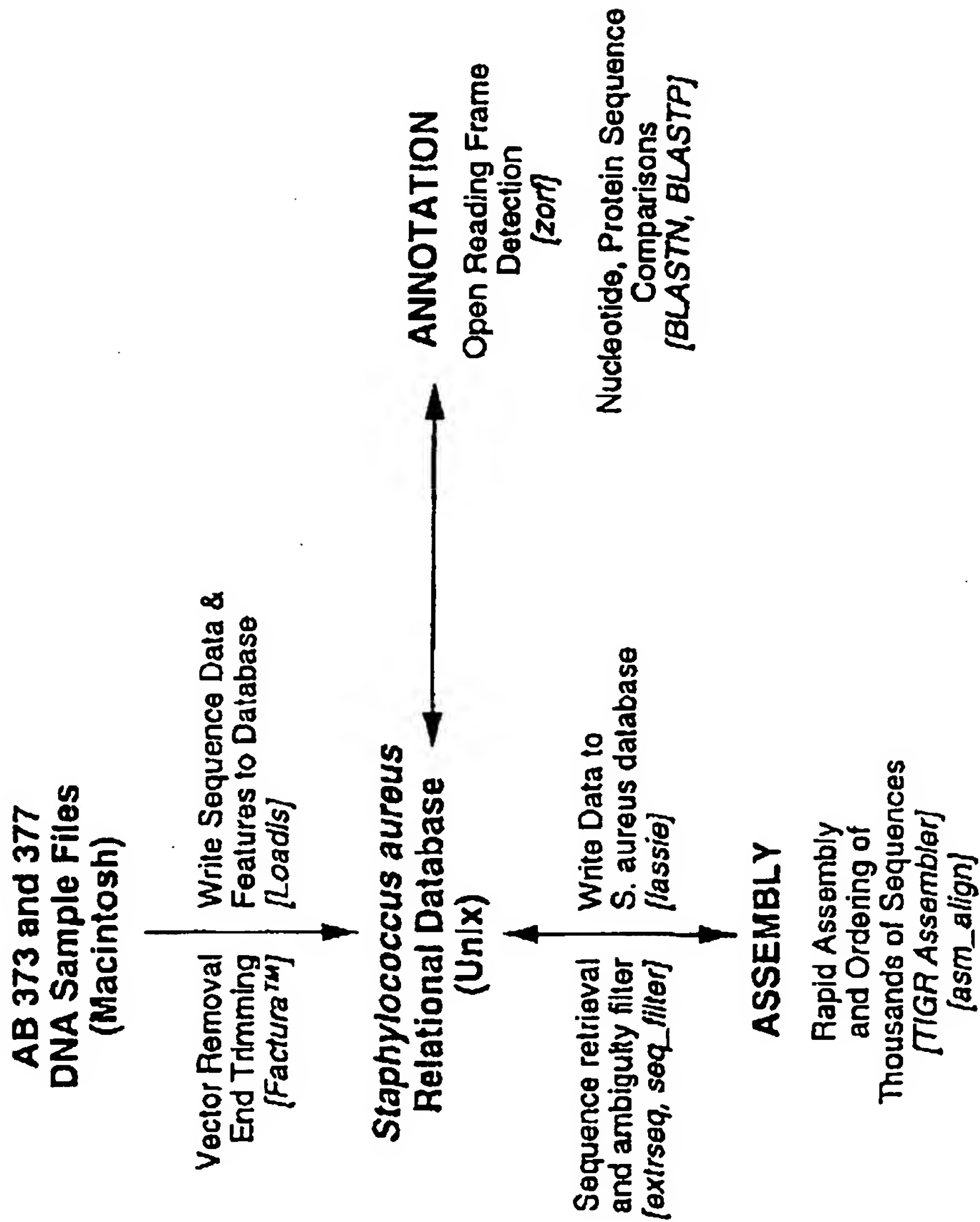


Figure 2



(12) **EUROPEAN PATENT APPLICATION**

(88) Date of publication A3:
14.10.1998 Bulletin 1998/42

(43) Date of publication A2:
30.07.1997 Bulletin 1997/31

(21) Application number: 97100117.7

(22) Date of filing: 07.01.1997

(51) Int Cl.⁶: **C12N 15/31**, G06F 17/30,
C12N 1/21, C12P 21/02,
C12Q 1/68, C07K 16/12,
C07K 14/31, A61K 39/085
// (C12N1/21, C12R1:445)

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC
NL PT SE
Designated Extension States:
AL LT LV RO SI

(30) Priority: 05.01.1996 US 9861

(71) Applicant: **HUMAN GENOME SCIENCES, INC.**
Rockville, MD 20850-3338 (US)

(72) Inventors:
• **Kunsch, Charles A.**
Gaithersburg, Maryland 20882 (US)

- **Choi, Gil H.**
Rockville, Maryland 20850 (US)
- **Barash, Steven C.**
Rockville, Maryland 20850 (US)
- **Dillon, Patrick J.**
Gaithersburg, Maryland 20879 (US)
- **Fannon, Michael R.**
Silver Spring, Maryland 20906 (US)
- **Rosen, Craig A.**
Laytonsville, Maryland 20882 (US)

(74) Representative: **VOSSIUS & PARTNER**
Postfach 86 07 67
81634 München (DE)

(54) **Staphylococcus aureus polynucleotides and sequences**

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynu-

cleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 97 10 0117 shall be considered, for the purposes of subsequent proceedings, as the European search report

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| Category | Citation of document with indication, where appropriate, of relevant passages | Relevant to claim | CLASSIFICATION OF THE APPLICATION (Int.Cl.6) |
| X | "EMBL Database entry SA5SRR, accession no. L36472, 17th November 1994, C.J. GREEN AND B.S. VOLD: "An unusual rRNA-tRNA gene organization in Staphylococcus aureus" EMBL NUCLEOTIDE SEQUENCE, XP002036821 --- | 1-29 | C12N15/31 G06F17/30 C12N1/21 C12P21/02 C12Q1/68 C07K16/12 C07K14/31 A61K39/085 /(C12N1/21, C12R1:445) |
| Y | BURKS C. ET AL.: "GenBank" NUCLEIC ACIDS RESEARCH., vol. 20, 1992, OXFORD GB, pages 2065-2069, XP002036820 * the whole document * | 1-29 | |
| Y | US 5 292 874 A (GEN-PROBE INC.) 8 March 1994 *whole document* | 1-29 | |
| Y | US 5 187 775 A (DNASTAR, INC.) 16 February 1993 *whole document* | 1-29 | |
| --- | | | |
| -/-- | | | |
| | | | TECHNICAL FIELDS SEARCHED (Int.Cl.6) |
| | | | C12N G06F C12P C12Q C07K A61K |
| INCOMPLETE SEARCH | | | |
| <p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>Article 52 (2)(d) EPC - Presentation of information - Claims 1-4 concerns computer readable media characterised solely by the information stored thereon. However, search has been carried out as far as possible.</p> | | | |
| Place of search | | Date of completion of the search | Examiner |
| MUNICH | | 31 July 1998 | Chakravarty, A |
| <p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p> | | | |

EPF FORM 1503 03.82 (P04C07)



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 97 10 0117

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | CLASSIFICATION OF THE APPLICATION (InLCI.6) |
|-------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|---------------------------------------------|
| Category | Citation of document with indication, where appropriate, of relevant passages | Relevant to claim | |
| Y | FLEISCHMANN R D ET AL: "WHOLE-GENOME RANDOM SEQUENCING AND ASSEMBLY OF HAEMOPHILUS INFLUENZAE RD" SCIENCE, vol. 269, no. 5223, 28 July 1995, pages 496-498, 507 - 512, XP000517090 * the whole document * | 1-29 | |
| X | --- DATABASE EMBL European Bioinformatics Institute Accession No. U21636, 21 November 1995 ZHANG Q. ET AL.: XP002073245 * abstract * | 1-29 | |
| X | --- DATABASE PIR Accession No. S15269, 13 January 1995 KONTINEN V.P. ET AL.: XP002073246 * abstract * | 1-29 | TECHNICAL FIELDS SEARCHED (InLCI.6) |
| X | --- DATABASE GENESEQ DERWENT Accession No. Q24523, 10 November 1992 YAMAZAKI H. ET AL.: XP002073247 * abstract * | 1-29 | |
| X | --- DATABASE PIR Accession No. S54820, 8 July 1995 MAHE B. ET AL.: XP002073248 * abstract * | 1-29 | |
| | --- -/-- | | |



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 97 10 0117

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | CLASSIFICATION OF THE APPLICATION (IntCl.6) |
|-------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|---------------------------------------------|
| Category | Citation of document with indication, where appropriate, of relevant passages | Relevant to claim | |
| X | DATABASE EMBL European Bioinformatics Institute Accession No. X56347, 6 March 1991 HOCH J.A.: XP002073249 * abstract * | 1-29 | |
| X | --- DATABASE PIR Accession number: A53310, 8 September 1995 TANIMOTO K. ET AL.: XP002073250 * abstract * | 1-29 | |
| X | --- DATABASE EMBL European Bioinformatics Institute Accession number: U38418, 9 December 1995 CHUNG Y.J. ET AL.: XP002073251 * abstract * | 1-29 | TECHNICAL FIELDS SEARCHED (IntCl.6) |
| A | --- DATABASE SWISSPROT Accession number: P33362, 1 February 1994 RICHTERICH P. ET AL.: XP002073252 * abstract * | 1-29 | |
| A | --- DATABASE PIR Accession number: S29683, 7 October 1994 GLASER P. ET AL.: XP002073253 * abstract * | 1-29 | |
| A | --- DATABASE PIR Accession number: S14508, 31 December 1991 SCHREIBER L. ET AL.: XP002073254 * abstract * | 1-29 | |
| | --- -/-- | | |



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 97 10 0117

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | CLASSIFICATION OF THE APPLICATION (Int.Cl.6) |
|-------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|----------------------------------------------|
| Category | Citation of document with indication, where appropriate, of relevant passages | Relevant to claim | |
| A | DATABASE PIR Accession number: Pc1253, 30 September 1993 STUCKA R. ET AL.: XP002073255 * abstract * | 1-29 | |
| A | --- DATABASE EMBL European Bioinformatics Institute Accession number: Z54398, 4 October 1995 ODELL. C ET AL.: XP002073256 * abstract * | 1-29 | |
| A | --- DATABASE EMBL European Bioinformatics Institute Accession number: U32788, 9 August 1995 FLEISCHMANN R.D. ET AL.: XP002073258 * abstract * | 1-29 | TECHNICAL FIELDS SEARCHED (Int.Cl.6) |
| A | --- DATABASE PIR Accession number: I64181, 18 August 1995 FLEISCHMANN ET AL.: XP002073259 * abstract * | 1-29 | |
| A | --- DATABASE EMBL European Bioinformatics Institute Accession number: U32744, 9 August 1995 FLEISCHMANN R.D. ET AL.: XP002073260 * abstract * | 1-29 | |
| | --- -/-- | | |



**European Patent
Office**

PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 97 10 0117

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | CLASSIFICATION OF THE APPLICATION (Int.Cl.6) |
|-------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|----------------------------------------------|
| Category | Citation of document with indication, where appropriate, of relevant passages | Relevant to claim | |
| A | <p>DATABASE PIR</p> <p>Accession number: P31728, 1 July 1993</p> <p>CHANYANGAM M. ET AL.:</p> <p>XP002073261</p> <p>* abstract *</p> <p>-----</p> | 1-29 | |
| | | | TECHNICAL FIELDS SEARCHED (Int.Cl.6) |
| | | | |
| | | | |